Discovery of methylated circulating DNA biomarkers for comprehensive non-invasive monitoring of treatment response in metastatic colorectal cancer

Discovery Of Methylated Circulating DNA Biomarkers For Comprehensive Non-Invasive Monitoring Of Treatment Response In Metastatic Colorectal Cancer.

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Short running head: Circulating methylated biomarkers for colorectal cancer monitoring

What is already known about this subject?

► Cancer mutations (eg, *BRAF*, *KRAS*, *TP53*), in cell-free circulating DNA could be used as markers of treatment response or disease relapse in patients with colorectal cancer but require prior knowledge of individual gene variants.

► DNA methylation alteration is a common early event in colorectal carcinogenesis and is detectable in cell-free circulating DNA; hence it was studied for early detection (eg, *SEPT9*) or tumour monitoring (eg, *NPY*, *WIF1*).

► Previous identification of methylated markers most often relied on assessment of few samples with low genome coverage methods and might have omitted important putative cancer-specific markers.

What are the new findings?

► Genome-wide DNA methylation analysis from stroma-free colorectal cancer cells identifies highly prevalent and specific methylated loci (*EYA4*, *GRIA4, ITGA4, MAP3K14-AS1* and *MSC*).

► Assessment of methylated markers in cell-free circulating DNA allows non-invasive monitoring of disease.

► DNA shedding of methylated markers is not impaired by treatment type or duration.

► Methylation changes over time correlate with tumour response evaluated by CT scan in patients with metastatic colorectal cancer treated with chemotherapy or targeted agents.

How might it impact on clinical practice in the foreseeable future?

► This panel of methylated markers was able to monitor tumour burden in patients with colorectal cancer treated with different conventional treatment regimens, including chemotherapy, anti-angiogenic agents and targeted agents. Liquid biopsy based on methylated markers could be coupled with imaging to improve timely therapeutic changes. This approach could also be useful for early pharmacodynamics assessments in clinical trials.

Abstract

Objective Mutations in cell-free circulating DNA (cfDNA) have been studied for tracking disease relapse in colorectal cancer (CRC). This approach requires personalised assay design due to the lack of universally mutated genes. In contrast, early methylation alterations are restricted to defined genomic loci allowing comprehensive assay design for population studies. Our objective was to identify cancer-specific methylated biomarkers which could be measured longitudinally in cfDNA (liquid biopsy) to monitor therapeutic outcome in patients with metastatic CRC (mCRC).

Design Genome-wide methylation microarrays of CRC cell lines (n=149) identified five cancer-specific methylated loci (EYA4, GRIA4, ITGA4, MAP3K14-AS1, MSC). Digital PCR assays were employed to measure methylation of these genes in tumour tissue DNA (n=82) and cfDNA from patients with mCRC (n=182). Plasma longitudinal assessment was performed in a patient subset treated with chemotherapy or targeted therapy.

Results Methylation in at least one marker was detected in all tumour tissue samples and in 156 mCRC patient cfDNA samples (85.7%). Plasma marker prevalence was 71.4% for EYA4, 68.5% for GRIA4, 69.7% for ITGA4, 69.1% for MAP3K14-AS1% and 65.1% for MSC. Dynamics of methylation markers was not affected by treatment type and correlated with objective tumour response and progression-free survival.

Conclusion This five-gene methylation panel can be used to circumvent the absence of patient-specific mutations for monitoring tumour burden dynamics in liquid biopsy under different therapeutic regimens. This method might be proposed for assessing pharmacodynamics in clinical trials or when conventional imaging has limitations.

Introduction

Tumours release fragments of nucleic acids into circulation, which could provide a minimally invasive surrogate for tissue biopsy as well as offering the opportunity of serial sampling over time.[1 2] Recent liquid biopsy studies have evaluated tumour-specific mutations or gene copy number changes in cell-free circulating DNA (cfDNA) derived from patients with digestive tract cancer for early diagnosis[3] and for monitoring the emergence of disease relapse.[1 4–7] This approach usually relied on alterations in oncogenic drivers such as *RAS* and *BRAF*—up to 50% of the colorectal cancer (CRC) population—or mutations within oncosuppressor genes (usually with no variant hotspots), therefore requiring specific assay design for each mutation. Studies mainly focused on follow-up after surgery[5 6 8] or on patients with CRC treated with epidermal growth factor receptor (EGFR) targeted therapies,[4 9 10] in which detection of oncogenic *RAS* alterations is associated with impaired treatment response. Changes in epigenetic patterns are often associated with alterations in physiological or pathological conditions triggering cell death and release of DNA with specific epigenetic marks,[11] which prompted exploring liquid biopsy tests as a surrogate of liver fibrosis severity in individuals affected by non-alcoholic fatty liver disease.[12] Changes in DNA methylation are considered an early event in carcinogenesis[13] and have already been proposed for early tumour detection in different settings (including CRC), allowing non-invasive population screening using stool[14 15] or blood.[16–21] The Food and Drug Administration recently approved the first blood test exclusively based on *SEPT9* methylation, which might lead to improvements in CRC screening uptake.[16 17] Here we propose the evaluation of DNA methylation markers in cfDNA, not as an early detection method, but rather as a non-invasive treatment-monitoring assay. Review of methylation markers for early detection of CRC identified genes which were highly tumour specific (not found in normal adjacent mucosa), but rarely validated in large cohorts.[22] While using innovative approaches and being very

informative, studies which aimed at identifying cancer-specific methylated markers usually relied on platforms with low genomic coverage,21 or small sample datasets,23 or exclusively assessed patient tissue18 24 which might have been partially infiltrated with stroma. We therefore employed genome-wide assessment of DNA methylation in a large collection of 149 CRC cell lines and identified a fivegene panel that was validated in tissue and cfDNA from patients with metastatic CRC (mCRC) using digital PCR-based assays (methyl-BEAMing19 25). Longitudinal assessment of this panel in cfDNA was performed to monitor disease burden in patients with mCRC over diverse treatment courses.

Materials and methods

Additional details are available in online supplementary file 1.

Cell lines and genome-wide DNA methylation data processing and retrieval

A collection of 149 cell lines of intestinal origin (see online supplementary file 2A) was assembled, as described.26 Infinium HumanMethylation450 BeadChip arrays were prepared according to manufacturer's protocol. Cell line methylation profiles are available on Gene Expression Omnibus (http:// www. ncbi. nlm. nih. gov/ geo/; accession number: GSE86078). After removing ulcerative colitis cases, cancer unrelated normal mucosa samples from GSE32146 were used as a control set. GSE41169 was employed as a blood control dataset (ie, healthy donors). GSE4275223 was used as a test cohort for establishing an in silico validation threshold. Level 1 data from the TCGA colorectal adenocarcinoma (COAD/READ) (https:// gdc- portal. nci. nih. gov) were used for the in silico validation. Further validation in normal tissues was performed using GSE48684.24

Data preprocessing and marker discovery analysis

All raw data (IDAT files) were preprocessed in R Bioconductor (minfi27). Probe signal was removed when the detection p value was above 0.05, or >1% of the dataset contained no

data, or if probes contained single nucleotide polymorphisms,28 demonstrated sexual dimorphism29 or were located on sex chromosomes. Our dataset was then merged with the other publicly available cohorts. Differential methylation analysis was performed at probe (lmFit from limma; adjusted p≤1×10-35; minimum delta beta-value of 0.8) or region level (bumphunter from minfi; threshold=0.8; regions represented by at least two probes with L≥2). Methylation in leucocytes was excluded (GSE41169; maximum beta-value allowed=0.1) to minimise the risk of false positivity in blood tests. Differentially methylated probes were limited to those overlapping differentially methylated regions, and 'liquid biopsy' assessable loci were defined as regions represented by at least two selected probes distant of a maximum 150 bp, the average fragment size reported in cfDNA30 and not located in centromeres or telomeres (see online Supplementary file 2B). Receiver operating characteristic analyses were performed in GSE42752 with the pROC package in R Bioconductor31 to establish thresholds, considering normal and adjacent mucosa as positive outcome and cancer as negative; only loci showing a threshold below 0.35 were kept. Each threshold was used to stratify the TCGA COAD/READ cohort, defining a positive predictive value (PPV) and negative predictive value (NPV) for discriminating normal adjacent from tumour tissue. Normal healthy and peritumoural samples from GSE4868424 were also controlled for absence of methylation above the threshold. All data used for the in silico analyses were from DNA derived from fresh frozen samples.

Methylation and genetic alteration assays for cfDNA evaluation

Assays were designed and optimised as described25 to allow methylation independent amplification. Full details are given in online supplementary file 2C and 3. In silico validation was performed using solely the probes which were located within the amplicon; results for the five markers of interest are displayed in online supplementary file 4. Evaluation of genetic alterations (*KRAS*, *BRAF* mutations and *MET* gene copy number) in

cfDNA was performed as reported.4 32 Assays, commercially available (Bio-Rad), are listed in online supplementary file 2C.

Tissue collection and DNA isolation

Formalin-fixed paraffin-embedded (FFPE) tissues originated from two different cohorts. The first consisted of macro-dissected tumour and normal adjacent tissues (n=31 cases; originating from several local hospitals), which were controlled for tumour purity and assembled at Niguarda Cancer Center, Grande Ospedale Metropolitano Niguarda (Milan, Italy) and from which DNA was newly extracted (average DNA concentration: 689 ng/µL (59–1844)). A second dataset of independent FFPE tumour tissues (n=51) was assembled from remaining DNA extracted during the enrolment of the DETECT-01 (EudraCT number 2011-002080- 21)33 or TEMECT (EudraCT number 2012-003338-17)34 trials (average DNA concentration: 163 ng/µL (10–776)).

Plasma collection and DNA isolation

De-identified plasma samples (average volume 1.5 mL (0.8–1.9)) from self-declared healthy donors (n=50) were purchased from the Brigham and Women's Hospital specimen bank (Boston, USA). One hundred and eighty-two mCRC cases were retrospectively enrolled in the study. One hundred and thirty-seven cases were selected for plasma time-points based on blood sample availability at a time when patients were presenting radiological evidence of disease. The remaining 45 cases were treatment baseline specimens, selected for availability of longitudinal follow-up samples (additional total of 132 longitudinal samples). The plasma volume obtained from patients with mCRC for the study was on average 1 mL (0.5–1.4). Summary of the clinicopathological features of the two cohorts can be found in online supplementary file 2D and patient clinical features are presented in online supplementary file 2E. mCRC plasma samples were collected at Niguarda Cancer Center, Grande Ospedale Metropolitano Niguarda (Milan, Italy) or at San Giovanni Battista Hospital (Turin, Italy). The study was conducted according to Good

Clinical Practices and was approved by the local ethics committee. Circulating DNA was extracted as previously described25 from 1 mL of plasma or less due to limited amount availability.

Statistics and data analyses

All methylation microarray analyses and figures were generated in R Bioconductor as previously mentioned. Prevalence and longitudinal representations were assembled in GraphPad. Wilcoxon test (for matched tissues analysis), Mann-Whitney U test and Kruskall-Wallis test (for group prevalence analyses) and Mantel-Cox log rank test (for survival analysis) were performed in GraphPad. Scatter matrix for marker correlation was obtained using OriginPro 2016 (OriginLab). All expressed p values were calculated with two-tailed tests and were considered significant when $p \leq 0.05$, unless otherwise specified.

Results

Marker selection and assay optimisation

Differential methylation analysis between CRC cell lines and normal mucosa identified 162 CpG dinucleotides representative of a larger genomic region controlled to be unmethylated in blood cells which represent the main contaminant source of cfDNA (figure 1, Supplementary file 2B and 5). Among the markers previously proposed for liquid biopsy assessment of CRC, *SEPT9* was discarded for few differentially methylated probes too distant from each other; *WIF1* was removed because of low differential methylation between normal and tumour tissue; while *NPY* demonstrated positivity in normal mucosa samples and blood cells (see online supplementary file 6). Thirty- nine loci defined by 93 probes, were selected as liquid biopsy assessable regions (see online supplementary file 5). An in silico validation (see online supplementary file 4), confirmed that the selected methylated loci were cancer specific and not a consequence of cell line establishment and identified six loci (five genes: *EYA4*, *GRIA4*, *ITGA4, MAP3K14-AS1, MSC*) capable of

discriminating cancer from normal mucosa with a PPV of 1 and a NPV above 0.5. Short methylation independent amplification was considered feasible for the five genes. Digital PCR (Methyl- BEAMing) assays were designed and their sensitivity and specificity were reassessed in silico using the probes located within the amplicon (see online supplementary file 4). The quantitative aspect of the assay was privileged over sensitivity, for better serving the purpose of monitoring tumour burden in advanced disease patients. Digital MIQE checklist can be found in online supplementary file 3.

Assessment of methylation markers in tissue from patients with CRC

Methylation status was evaluated in FFPE tissue DNA for the five markers defined above (*EYA4*, *GRIA4*, *ITGA4*, *MAP3K14-AS1, MSC*). Amplification was successful in all cases. Significantly higher methylation levels were observed in tumour tissue compared with their normal counterpart ($p<0.0001$), and remained high in an independent set of non-macro-dissected tumour specimens (figure 2). Average methylation (and range) for normal tissues was 0.6% (0–3), 7.9% (0–28), 0.5% (0–9), 0.3% (0–2) and 2.3% (0–12) for *EYA4*, *GRIA4*, *ITGA4*, *MAP3K14-AS1, MSC,* respectively. Average methylation (and range) for matched tumour tissues was 42.2% (0–92), 67.1% (18–97), 51.7% (2–96), 43.5% (0–97) and 71.5% (31–97) for *EYA4*, *GRIA4*, *ITGA4*, *MAP3K14-AS1, MSC,* respectively.

Detection of methylation markers in cfDNA of healthy individuals and patients with CRC

Plasma samples were obtained from a cohort of self-declared healthy individuals deliberately chosen above age 40 (n=50), and from a cohort of patients with mCRC (n=182). Methylation status was evaluated in a total of 364 cfDNA samples for the five markers (Figure 1 and online supplementary file 2G). Amplification was successful in all samples but one for *GRIA4* (0.3%), four cases for *ITGA4* (1.1%) and seven for *MSC* (1.9%) (online supplementary file 2G).

Marker prevalence in cfDNA

Considering only non-longitudinal mCRC samples from individual patients for prevalence purpose (figure 1), all markers showed significant differences in methylation distribution between self-declared healthy donors and patients with mCRC (U test: p<0.0001, Figure 3A–E and online supplementary file 2G). Average methylation (and range) for self-declared healthy donors was 0.5% (0–7.8), 0.5% (0–17), 0.2% (0–2.2), 0% (0–0.2) and 0% (0–0.6) for *EYA4*, *GRIA4*, *ITGA4*, *MAP3K14-AS1, MSC,* respectively. Average methylation (and range) for non-longitudinal mCRC samples was 26.2% (0–98.4), 33.5% (0–99.7), 33.2% (0–99), 26.3% (0–100) and 37.9% (0–100) for *EYA4*, *GRIA4*, *ITGA4*, *MAP3K14-AS1, MSC,* respectively. Receiver operating characteristic curve (ROC) analyses were performed for each marker in order to evaluate their performance and establish a clinically relevant positivity threshold to discriminate self-declared healthy donors from patients with mCRC (see online Supplementary file 7). Cut-off values were 0.7% for *EYA4*, 0.79% for *GRIA4*, 1.06% for *ITGA4,* 0.24% for *MAP3K14-AS1*, 0.9% for *MSC* and 0.68% when averaging the five markers. Only two plasma samples from healthy donors showed an average methylation above the threshold (Figure 3G). This was due to high methylation values in *GRIA4* and *EYA4* for one individual (aged 43 years), and in *EYA4* for the second (aged 62 years). One hundred and thirty-nine (76%) patients with mCRC displayed an average methylation above the threshold. Positivity, defined as the methylation value over cut-off thresholds and number of methylated events above the limit of blank (LOB), was observed in 71.4% for *EYA4*, 68.5% for *GRIA4*, 69.7% for *ITGA4*, 68.1% for *MAP3K14-AS1*, 65.1% for *MSC*, respectively. Considering that positivity in a single marker would be enough to track tumour burden, we evaluated that 156 cases (86%) showed positivity in at least one marker. When methylation values were positive, all markers were correlated (figure 3H and online Supplementary file 8). Total DNA amount assessed by genome equivalent per millilitre also significantly discriminated self-declared healthy donors from

patients with mCRC, although with lower specificity (Figure 3F and online Supplementary file 7).

Marker prevalence in tumour tissue and matched metachronous cfDNA samples

Tumour tissue DNA and matched metachronous cfDNA samples were available for a small subset of patients for which primary tumour had been resected (n=39). Marker negativity in cfDNA samples was not explained by absence of methylation in the matched tumour tissue counterpart (see online Supplementary file 9).

Association between cfDNA methylation and clinicopathological features

Using univariate analyses, age, treatment status and *BRAF* or *RAS* oncogenic mutations were not associated with different methylation values (see online Supplementary file 10; Supplementary file 2). High carcinoembryonic antigen (CEA) level (>5 ng/mL) showed a non-significant trend for higher methylation values in cfDNA (p=0.11). Male gender was significantly associated with lower methylation values (p=0.029), while the presence of unresected primary tumour (p=0.002), bulky disease (defined as massive tumour involvement of >50% of liver or lungs; p=0.012) or multiple metastatic lesions (p=0.023) were significantly associated with higher methylation values. The sum of target lesions as *per* Response Evaluation Criteria for Solid Tumours (RECIST)35 from available CT scans was also associated with high methylation in the highest quartiles. Altogether these findings strongly suggest an association between release of methylated cfDNA and tumour burden.

Longitudinal assessment

Among the 182 patients with mCRC, 45 were followed-up longitudinally (figure 1); of those, seven were excluded due to absence of any positive marker at baseline (n=6) or inadequate follow-up (n=1). Methylation changes, between baseline and longitudinal plasma samples (obtained within 20 days from the first radiological evaluation) were annotated with the tumour response status to therapy (see online Supplementary file 11).

Significant lower methylation values were detected in samples collected close to radiological assessment of clinical benefit (defined as objective disease stabilisation or partial response as per RECIST criteria) for all markers but *EYA4*. In comparison, samples collected close to documented objective tumour progression showed a non-significant trend towards increased methylation values for all markers. This suggests that cfDNA methylation changes could be associated with tumour burden dynamics. Therefore, we investigated whether longitudinal follow-up of methylation could track tumour burden over time. For this purpose, for each longitudinal time-point an average of selected markers (ASM) was calculated based exclusively on the loci which displayed positive methylation in the baseline.

Monitoring of mCRC response to conventional chemotherapy

Ten cases received conventional chemotherapy regimens (FOLFOX, FOLFIRI, with or without bevacizumab). Two cases were excluded because they were negative at baseline. All patients carried *KRAS* or *BRAF* mutated tumours (considered as early events in tumourigenesis) allowing correlative assessment with methylation (figure 4). ASM was used for longitudinal monitoring. For most time-points, ASM dynamics recapitulated tumour burden changes as assessed by imaging, with a decrease preceding partial response or stable disease, while an increase or stable ASM anticipated progression. For all cases with known mutations in the corresponding tissue, *KRAS* or *BRAF* mutant levels in cfDNA paralleled the ASM. At a few time-points negative for mutation detection and displaying low DNA amount, ASM was around 1%, which could reflect either higher sensitivity of multiple methylated marker testing or possible overestimation of the current assays (see online Supplementary file 12).

Monitoring of mCRC response to targeted therapy

Additional six cases with longitudinal follow-up were treated with the EGFR targeted antibody panitumumab based on *RAS* wild-type status (figure 1). One case displaying a

baseline sample negative for methylation was excluded. Four out of five cases (figure 5) demonstrated emergence of a resistance causative alteration at progression which could be retrospectively analysed over time. In three individuals, progression was associated with the emergence of *KRAS* alterations (figure 5A-C),4 in one by *MET* gene amplification32 (figure 5D). In all cases, ASM increased in parallel with the emergence of the resistance causative alteration. However, ASM values in plasma were much more abundant than the percentage of mutant *KRAS* alleles in two cases. In two patients, panitumumab was followed at progression by standard chemotherapy (irinotecan) that was associated with decrease of *KRAS* cfDNA level independently of the methylation dynamics. The remaining case for which the molecular mechanism of resistance to EGFR target therapy remained unexplained could still be monitored in cfDNA with an increase in the ASM value at progression (figure 5E).

Application of methylated circulating DNA monitoring in a clinical trial with temozolomide in chemorefractory mCRC with MGMT hypermethylation

We investigated the use of methylated cfDNA in 29 cases from the TEMECT trial (EudraCT number 2012-003338-17), which assessed efficacy of temozolomide treatment in patients with chemorefractory mCRC selected based on their O-6-methylguanine- DNA methyltransferase (MGMT) methylated status in the primary tumour tissue.34 Three cases without any positive methylated marker at baseline and one case without longitudinal collection were excluded (figure 1). To explore whether methylated markers in liquid biopsy could be used as a surrogate to imaging, we considered the best methylation change over time, similarly to what is usually performed with imaging-based RECIST criteria. To this aim, the ASM at a longitudinal timepoint was subtracted from the ASM value at baseline, and the best methylation change (lowest) over the course of treatment was selected for correlative assessment with radiological response (see online supplementary file 2l). A decrease in methylation was associated with clinical benefit as

evaluated by RECIST (stable disease or partial response; figure 6A, PPV=0.82; NPV=0.79, p=0.0048). Considering the best ASM change over time, a decrease in ASM was associated with improved progression-free survival (p=0.039, HRrelapse=0.48 (0.17–0.87); figure 6B).

Discussion

The current use of imaging for follow-up in CRC suffers from limitations potentially leading to overtreatment, delays in treatment reorientation and potential side effects of exposure to imaging contrast agents. The evaluation of serum protein levels such as CEA offers a rapid and cost-effective way to measure disease evolution, but is impaired by limited sensitivity and specificity, the latter especially during treatment courses due to inflammation and release of protein in the bloodstream.36 Furthermore, a fraction of patients with mCRC does not show detectable plasmatic CEA levels during the natural history of the disease.37 Longitudinal evaluation of cancer-specific mutations in cfDNA has been exploited to identify relapse after surgery5 or during treatment with both standard chemotherapies and targeted agents,1 4 and it demonstrated great specificity and sensitivity. However, these studies must rely on either mutational hotspots with partial prevalence (only up to 50% considering all alterations of *KRAS* and *BRAF*) or on personalised assay design after identification of a variant through massive parallel sequencing.4 5 Alterations in methylation patterns present an advantage, as they are limited to specific regions of the genome, allowing for a universal assay design compatible for population studies. Moreover, their prevalence is usually high, which triggered their implementation as early diagnostic assays.38 We confirmed the proof-of-concept work from Garrigou *et al*39 that DNA methylation in cfDNA may be employed to track response during therapy in mCRC, enabling non-invasive monitoring of tumour burden. To go beyond previous efforts in this area, we decided to perform a marker discovery analysis

using CRC cell lines. This strategy allowed removal of background signal coming from stroma, which has recently been described to impair cancer signal specificity in genome-wide analyses.[40] Further validation in independent cohorts (in silico) or in tissue samples confirmed that these markers were cancer specific and not a consequence of cell line establishment. To our knowledge, only two studies from the same group evaluated methylation markers dynamics in mCRC cases on treatment.[39 41] In their manuscript, Garrigou *et al* detected methylation of *WIF1* and *NPY* by liquid biopsy in 80% mCRC, and evaluated their levels over time in cfDNA from three mCRC cases under chemotherapy treatment.[39] In a follow-up study, combining *WIF1* and *NPY* methylation Garlan *et al* showed 69.2% positivity in KRAS/BRAF/TP53 wild-type mCRC.[41] While these markers were identified by Roperch *et al*[21] using the Illumina GoldenGate methylation arrays (lower coverage than the Illumina Infinium), they were sorted out from our pipeline. *NPY* was discarded due to positivity in normal mucosa and in whole blood samples which contain white blood cells as the main contaminant of cfDNA. *WIF1* instead did not satisfy our stringent threshold criteria due to limited differential methylation between normal healthy/normal adjacent mucosa and tumour. Methylation of *WIF1* in normal mucosa was previously described in a small dataset[42] warranting further investigation to verify the specificity of this marker. Among other established liquid biopsy markers for CRC, *SEPT9* was also filtered out from the analysis due to distance between the significantly differentially methylated probes above the 150 bp threshold. Among the methylated loci identified in our work, *EYA4* and *ITGA4* are known or putative tumour suppressor genes,[43–46] while the functional role of the other markers -*GRIA4*, *MSC* and *MAP3K14-AS1*- in carcinogenesis remains to be elucidated; however, their in silico validation in independent cohorts as well as in tissue demonstrated their reliability in identifying tumour cells. Comparing cfDNA samples from self-declared healthy donors to patients with mCRC, all markers showed specificity above 0.85. The less efficient marker was *EYA4*, which

demonstrated low methylated values in all donor samples. Since the signal was higher than the LOB of the assay, we hypothesised that this could be attributed to age-related methylation in normal tissue. When evaluating plasma samples of patients with cancer, we established positivity as methylation value above a ROC threshold (allowing the best discrimination between healthy individuals and patients with cancer) and signal with positive events above the LOB. While these detection thresholds efficiently define the marker(s) to be followed over time, these assays are still suboptimal for other purposes such as early detection or minimal residual disease assesment. Despite heterogeneity among patients, the high prevalence of at least one methylated marker warrants including these loci in a panel as a blood test for detection of plasma DNA of tumour origin in patients with stage IV CRC. In our setting, all cases with intact primary CRC in situ displayed at least one positive methylation marker, confirming that cases in which primary lesions were not resected could be more efficiently tracked through liquid biopsy. As seen for *SEPT9*,47 there was a positive correlation between cfDNA concentrations—here measured by genome equivalent per millilitre of plasma—and average methylation. However, in some samples with low total DNA content (below 20 000 genome equivalent), high methylation values were recorded; on the other hand, a subset of samples with high genome equivalent did not display detectable methylation in the selected loci. We hypothesise that these discrepancies could be explained by haemolysis during sample preparation and consequent contamination of plasma by leucocyte DNA, or by release of DNA from non-cancerous tissues during treatment, possibly due to inflammation or hepatotoxicity. Individual markers had prevalence around 65%, and only combining the positivity of all five methylated loci resulted in 86% overall prevalence, which is slightly higher but similar to what previously reported when both *NPY* and *WIF1* were assessed in the metastatic setting.39 Yet, there were still 14% of mCRC cfDNA samples with undetectable circulating DNA methylation, which warrants further studies investigating

possible biological or technical bases. None of the recorded clinicopathological features correlated with lack of detectable methylation levels in cfDNA. Indeed, in our limited subset of matched tissue and plasma samples, marker negativity in cfDNA was not related to low methylation value in tumour tissue DNA. Consequently, we speculate that this discordance between sample types could be attributed to spatial or temporal intratumour epigenetic heterogeneity, 48 limited DNA shedding into circulation or suboptimal plasma specimen handling. Since tissue and microarray data displayed very low rate of non-methylated template (0% in our tissue dataset; 1.1% in microarray data), we expect that technical improvements at the detection level as well as at the DNA isolation level (eg, using higher plasma volume), will be required to achieve full penetrance of the assay. In addition to *NPY* and *WIF1*, other previously identified methylated loci in genes such as *SEPT9*,16 49 *VIM*19 or *C9ORF50*18 are amenable to liquid biopsy analyses, and their use in combination with our panel might also improve the positivity of cfDNA detection. One self-declared healthy donor displayed positivity in two markers and high GE content, possibly suggesting either a false-positive result or that this individual had an asymptomatic neoplastic lesion. However, the sample collection process (ie, de-identification) prevented us from verifying this hypothesis. It should be acknowledged that our digital PCR-based approach was not designed as a cancer diagnostic test, but rather optimised for its linearity and quantification ability of methylated DNA in advanced disease. Nevertheless, future studies are warranted to establish the methylation status and prevalence of the markers identified by our study in the earlier stages of colorectal neoplastic disease. This knowledge together with the development of assays that would privilege sensitivity over quantification are key to establish whether these findings could be relevant also in the setting of early detection. There was good correlation (above 0.55) between levels of circulating DNA methylation and early genetic events in colorectal tumourigenesis such as *KRAS* or *BRAF* mutations, which validates the possibility to use methylation without prior

knowledge of the tumour genetic pattern, as previously shown.[39 41] Of note, four samples involved in the study were also assessed by massive parallel sequencing (data not shown) and presented genetic mutations at an allelic frequency comparable to the percentage of methylated markers, which highlights a possible role of our panel for plasma quality assessment prior to sequencing. In fact, massive parallel sequencing sometimes fails to detect tumour-specific somatic mutations due to low tumour content in cfDNA and methylation assay could therefore be used for checking tumour DNA enrichment in plasma as a quality control step. Methylation markers in cfDNA of patients treated with EGFR inhibitors, paralleled the emergence of resistance causative genetic alterations. This finding suggests the possibility to use these methylation markers as whole tumour DNA content normaliser in plasma. This will be of particular importance when qualitative assessment (presence or absence) of individual mutation variants in the blood is not enough to predict response. Interestingly, in two cases, the likely resistance mechanism (*KRAS* alteration) showed very low mutant allelic frequency in comparison to the estimated amount of tumour derived cfDNA (as judged by ASM). We hypothesised that either the tumour harboured additional unknown mechanisms of resistance or a small fraction of *KRAS* altered cells was enough to protect the main bulk of the neoplastic lesion via paracrine effectors as previously demonstrated.[50] In two cases that progressed through emergence of a *KRAS* mutation, levels of mutant alleles decreased on treatment with irinotecan, independently of methylation, suggesting that the fitness of *KRAS* mutant clones is dependent on the presence of anti-EGFR antibodies, as previously proposed.[4] To our knowledge, very few studies evaluated longitudinally methylated cfDNA,[39 41 51] and most works essentially focused on analysis of pretreatment samples to find predictive markers of response. Here, we showed that evolution of the methylation abundance over time demonstrated good prediction of response status during treatment with conventional therapies for mCRC. This suggests that longitudinal assessment of methylation could be

used in between radiological assessments for more accurate follow-up of the disease. We were also able to retrospectively assess a batch of samples that were collected in a clinical trial with temozolomide for the treatment of chemorefractory mCRC. Samples were not collected with the aim to directly compare cfDNA with CT scans. Imaging was not usually performed at the very same time-points when blood was drawn. Despite this limitation and the low response rate of mCRC on temozolomide treatment, dynamics of methylation could predict clinical benefit. This implicates that the monitoring of methylated circulating DNA might be used as a surrogate to imaging in order to evaluate treatment efficacy and might help reducing delays in therapeutic reorientation. In fact, with the emergence of concepts such as early tumour shrinkage associated with long-term outcome,[52 53] short-term evaluation of pharmacodynamic response using liquid biopsy might become common practice. In summary, we presented here a panel of five methylated universal markers of circulating DNA of tumour origin that can be efficiently used to monitor advanced CRC on most currently available treatments. We hypothesise that combining radiological and repetitive cfDNA assessments will improve monitoring of patients with mCRC and would help clinicians to adjust treatment more efficiently by adopting more timely surgical intervention or early therapeutic reorientation.

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Contributors

LB, AB, ASB and FDN participated in the design of the study. AA, AP, AC, ABi, CCr, SB, KB, PR, KBM, SS and ASB contributed to the collection and retrieval of clinical data of blood samples. AA, AC, AV, MT, SS and ASB contributed to the collection and retrieval of tissue samples. LB, AP, CF, CCr, AC, BM, GS and DO contributed to blood sample preparation and processing. LB, SMo, SMa, SG, GM, WG and ME contributed to the genome-wide methylation experiments. PZ contributed to establishing the pipeline for in silico and wet validation of GRIA4. LB performed the bioinformatics analyses of the genome-wide methylation experiments. LB, CF and DO performed methylation analyses in cfDNA samples. BM and GS performed genetic alteration analyses in cfDNA samples. LB, BM and GS interpreted the results in cfDNA. LB and FDN wrote the manuscript. All authors critically reviewed and commented the manuscript.

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Competing interests

AB reports personal fees (scientific advisory board member) from Horizon Discovery, personal fees (scientific advisory board member) from Biocartis, personal fees (Consultant) from Novartis, personal fees (Consultant) from Roche, personal fees (Consultant) from Illumina. AB and FDN reports grants from Trovagene, outside the submitted work. In addition, FDN and PZ have a patent 102017000072650 pending. All the other authors have nothing to disclose.

Ethics approval

Niguarda Cancer Center ethics commitee; San Giovanni Battista Hospital ethics commitee.

Provenance and peer review

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Author note

AS-B and FDN contributed equally as co-senior authors.

References

1 Bettegowda C, Sausen M, Leary RJ, et al. Detection of circulating tumor DNA in earlyand late-stage human malignancies. Sci Transl Med 2014;6:ra24.

2 Crowley E, Di Nicolantonio F, Loupakis F, et al. Liquid biopsy: monitoring cancergenetics in the blood. Nat Rev Clin Oncol 2013;10:472–84.

3 Berger AW, Schwerdel D, Costa IG, et al. Detection of hot-spot mutations in circulating cell-free DNA from patients with intraductal papillary mucinous neoplasms of the pancreas. Gastroenterology 2016;151:267–70.

4 Siravegna G, Mussolin B, Buscarino M, et al. Clonal evolution and resistance to EGFR blockade in the blood of colorectal cancer patients. Nat Med 2015;21:827.

5 Tie J, Wang Y, Tomasetti C, et al. Circulating tumor DNA analysis detects minimal residual disease and predicts recurrence in patients with stage II colon cancer. Sci Transl Med 2016;8:346ra92.

6 Reinert T, Scholer LV, Thomsen R, et al. Analysis of circulating tumour DNA to monitor disease burden following colorectal cancer surgery. Gut 2016;65:625–34.

7 Berger AW, Schwerdel D, Welz H, et al. Treatment monitoring in metastatic colorectal cancer patients by quantification and KRAS genotyping of circulating cell-free DNA. PLoS One 2017;12:e0174308.

8 Diehl F, Schmidt K, Choti MA, et al. Circulating mutant DNA to assess tumor dynamics. Nat Med 2008;14:985–90.

9 Spindler KL, Pallisgaard N, Appelt AL, et al. Clinical utility of KRAS status in circulating plasma DNA compared to archival tumour tissue from patients with metastatic colorectal cancer treated with anti-epidermal growth factor receptor therapy. Eur J Cancer 2015;51:2678–85.

10 Taly V, Pekin D, Benhaim L, et al. Multiplex picodroplet digital PCR to detect KRAS mutations in circulating DNA from the plasma of colorectal cancer patients. Clin Chem 2013;59:1722–31.

11 Lehmann-Werman R, Neiman D, Zemmour H, et al. Identification of tissue-specific cell death using methylation patterns of circulating DNA. Proc Natl Acad Sci U S A 2016;113:E1826–E1834.

12 Hardy T, Zeybel M, Day CP, et al. Plasma DNA methylation: a potential biomarker for stratification of liver fibrosis in non-alcoholic fatty liver disease. Gut 2017;66:1321–8.

13 Baylin SB, Jones PA. A decade of exploring the cancer epigenome - biological and translational implications. Nat Rev Cancer 2011;11:726–34.

14 Chen WD, Han ZJ, Skoletsky J, et al. Detection in fecal DNA of colon cancer-specific methylation of the nonexpressed vimentin gene. J Natl Cancer Inst 2005;97:1124–32.

15 Imperiale TF, Ransohoff DF, Itzkowitz SH, et al. Multitarget stool DNA testing for colorectal-cancer screening. N Engl J Med 2014;370:1287–97.

16 Warren JD, Xiong W, Bunker AM, et al. Septin 9 methylated DNA is a sensitive and specific blood test for colorectal cancer. BMC Med 2011;9:133.

17 Church TR, Wandell M, Lofton-Day C, et al. Prospective evaluation of methylated SEPT9 in plasma for detection of asymptomatic colorectal cancer. Gut 2014;63:317–25.

18 Lange CP, Campan M, Hinoue T, et al. Genome-scale discovery of DNA-methylation biomarkers for blood-based detection of colorectal cancer. PLoS One 2012;7:e50266.

19 Li M, Chen WD, Papadopoulos N, et al. Sensitive digital quantification of DNA methylation in clinical samples. Nat Biotechnol 2009;27:858–63.

20 Young GP, Pedersen SK, Mansfield S, et al. A cross-sectional study comparing a blood test for methylated BCAT1 and IKZF1 tumor-derived DNA with CEA for detection of recurrent colorectal cancer. Cancer Med 2016;5:2763–72.

21 Roperch JP, Incitti R, Forbin S, et al. Aberrant methylation of NPY, PENK, and WIF1 as a promising marker for blood-based diagnosis of colorectal cancer. BMC Cancer 2013;13:566.

22 Xue M, Lai SC, Xu ZP, Zp X, et al. Noninvasive DNA methylation biomarkers in colorectal cancer: A systematic review. J Dig Dis 2015;16:699–712.

23 Naumov VA, Generozov EV, Zaharjevskaya NB, et al. Genome-scale analysis of DNA methylation in colorectal cancer using infinium humanmethylation450 beadchips. Epigenetics 2013;8:921–34.

24 Luo Y, Wong CJ, Kaz AM, et al. Differences in DNA methylation signatures reveal multiple pathways of progression from adenoma to colorectal cancer. Gastroenterology 2014;147:418–29.

25 Barault L, Amatu A, Bleeker FE, et al. Digital PCR quantification of MGMT methylation refines prediction of clinical benefit from alkylating agents in glioblastoma and metastatic colorectal cancer. Ann Oncol 2015;26:1994–9.

26 Medico E, Russo M, Picco G, et al. The molecular landscape of colorectal cancer cell lines unveils clinically actionable kinase targets. Nat Commun 2015;6:7002.

27 Aryee MJ, Jaffe AE, Corrada-Bravo H, et al. Minfi: a flexible and comprehensive bioconductor package for the analysis of Infinium DNA methylation microarrays. Bioinformatics 2014;30:1363–9.

28 Price ME, Cotton AM, Lam LL, et al. Additional annotation enhances potential for biologically-relevant analysis of the illumina infinium humanmethylation450 beadchip array. Epigenetics Chromatin 2013;6:4.

29 Chen YA, Lemire M, Choufani S, et al. Discovery of cross-reactive probes and polymorphic CpGs in the illumina infinium humanmethylation450 microarray. Epigenetics 2013;8:203–9.

30 Schwarzenbach H, Hoon DS, Pantel K. Cell-free nucleic acids as biomarkers in cancer patients. Nat Rev Cancer 2011;11:426–37.

31 Robin X, Turck N, Hainard A, et al. pROC: an open-source package for R and S+ to analyze and compare ROC curves. BMC Bioinformatics 2011;12:77.

32 Bardelli A, Corso S, Bertotti A, et al. Amplification of the MET receptor drives resistance to anti-EGFR therapies in colorectal cancer. Cancer Discov 2013;3:658–73. 33 Amatu A, Sartore-Bianchi A, Moutinho C, et al. Promoter CpG island hypermethylation of the DNA repair enzyme MGMT predicts clinical response to dacarbazine in a phase II study for metastatic colorectal cancer. Clin Cancer Res 2013;19:2265–72.

34 Amatu A, Barault L, Moutinho C, et al. Tumor MGMT promoter hypermethylation changes over time limit temozolomide efficacy in a phase II trial for metastatic colorectal cancer. Ann Oncol 2016;27:1062–7.

35 Eisenhauer EA, Therasse P, Bogaerts J, et al. New response evaluation criteria in solid tumours: revised RECIST guideline (version 1.1). Eur J Cancer 2009;45:228–47.

36 Lech G, Słotwiński R, Słodkowski M, et al. Colorectal cancer tumour markers and biomarkers: recent therapeutic advances. World J Gastroenterol 2016;22:1745–55.

37 Nicholson BD, Shinkins B, Pathiraja I, et al. Blood CEA levels for detecting recurrent colorectal cancer. Cochrane Database Syst Rev 2015;12:CD011134.

38 Laird PW. The power and the promise of DNA methylation markers. Nat Rev Cancer 2003;3:253–66.

39 Garrigou S, Perkins G, Garlan F, et al. A study of hypermethylated circulating tumor DNA as a universal colorectal cancer biomarker. Clin Chem 2016;62:1129–39.

40 Isella C, Terrasi A, Bellomo SE, et al. Stromal contribution to the colorectal cancer transcriptome. Nat Genet 2015;47:312–9.

41 Garlan F, Laurent-Puig P, Sefrioui D, et al. Early Evaluation of Circulating Tumor DNA as Marker of Therapeutic Efficacy in Metastatic Colorectal Cancer Patients (PLACOL Study). Clin Cancer Res 2017;23:5416–25.

42 Patai ÁV, Valcz G, Hollósi P, et al. Comprehensive DNA methylation analysis reveals a common ten-gene methylation signature in colorectal adenomas and carcinomas. PLoS One 2015;10:e0133836.

43 De Carvalho DD, Sharma S, You JS, et al. DNA methylation screening identifies driver epigenetic events of cancer cell survival. Cancer Cell 2012;21:655–67.

44 Kim SJ, Tae CH, Hong SN, et al. EYA4 Acts as a new tumor suppressor gene in colorectal cancer. Mol Carcinog 2015;54:1748–57.

45 Ausch C, Kim YH, Tsuchiya KD, et al. Comparative analysis of PCR-based biomarker assay methods for colorectal polyp detection from fecal DNA. Clin Chem 2009;55:1559–63.

46 Chang E, Park DI, Kim YJ, et al. Detection of colorectal neoplasm using promoter methylation of ITGA4, SFRP2, and p16 in stool samples: a preliminary report in Korean patients. Hepatogastroenterology 2010;57:720–7.

47 Tóth K, Wasserkort R, Sipos F, et al. Detection of methylated septin 9 in tissue and plasma of colorectal patients with neoplasia and the relationship to the amount of circulating cell-free DNA. PLoS One 2014;9:e115415.

48 Martínez-Cardús A, Moran S, Musulen E, et al. Epigenetic homogeneity within colorectal tumors predicts shorter relapse-free and overall survival times for patients with locoregional cancer. Gastroenterology 2016;151:961–72.

49 Wasserkort R, Kalmar A, Valcz G, et al. Aberrant septin 9 DNA methylation in colorectal cancer is restricted to a single CpG island. BMC Cancer 2013;13:398.

50 Hobor S, Van Emburgh BO, Crowley E, et al. TGFα and amphiregulin paracrine network promotes resistance to EGFR blockade in colorectal cancer cells. Clin Cancer Res 2014;20:6429–38.

51 Fackler MJ, Lopez Bujanda Z, Umbricht C, et al. Novel methylated biomarkers and a robust assay to detect circulating tumor DNA in metastatic breast cancer. Cancer Res 2014;74:2160–70.

52 Cremolini C, Loupakis F, Antoniotti C, et al. Early tumor shrinkage and depth of response predict long-term outcome in metastatic colorectal cancer patients treated with first-line chemotherapy plus bevacizumab: results from phase III TRIBE trial by the Gruppo Oncologico del Nord Ovest. Ann Oncol 2015;26:1188–94.

53 Douillard JY, Siena S, Peeters M, et al. Impact of early tumour shrinkage and resection on outcomes in patients with wild-type RAS metastatic colorectal cancer. Eur J Cancer 2015;51:1231–42.

Figures

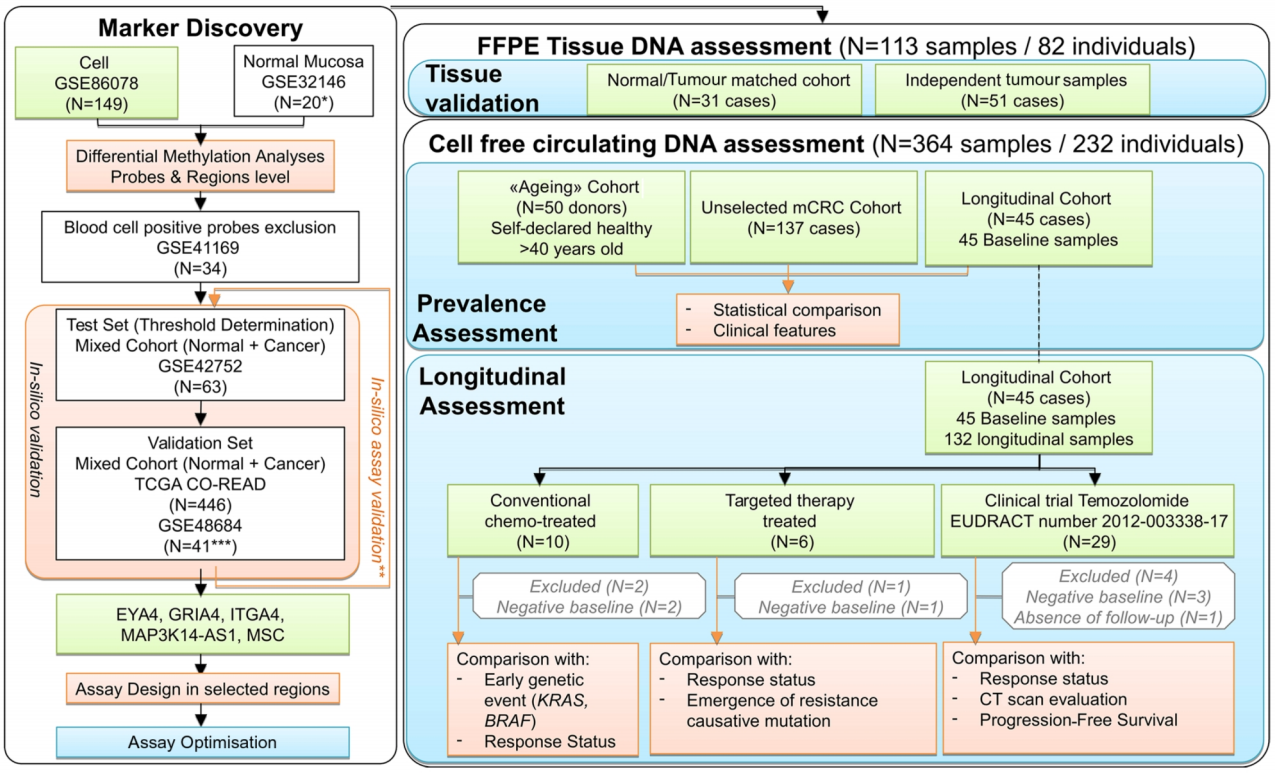

Figure 1 Workflow of the study. A multistep marker discovery analysis was first performed to identify highly prevalent cancer-specific markers. After design, assay probes were further validated in silico. Assays were optimised to achieve linear quantification over a wide methylation range (0.09%– 100%). Marker prevalence was first evaluated in tissue samples from 82 subjects with CRC. Then marker prevalence was evaluated in cfDNA in a total of 232 donors enrolled in the study among which 50 were de-identified self-declared healthy donors, and 182 patients with mCRC. Among mCRC cases, 45 were followed longitudinally and treated either with conventional chemotherapy, targeted therapy regimen or with temozolomide (TMZ) as part of a clinical trial. Methylation was analysed longitudinally for cases with positivity in at least one marker at baseline sample. Methylation dynamics was then compared with additional available clinical or molecular features. In green: unpublished data; in blue: bench experiments; in orange: bioinformatics or statistical analyses with clinical correlates; in grey: sample exclusion. *GSE32146 was used after removal of ulcerative colitis cases. **In silico validation was performed again

restricting the analysis to the probes included in the assay amplicon. ***Only normal healthy and peritumoural tissues were used from GSE48684.

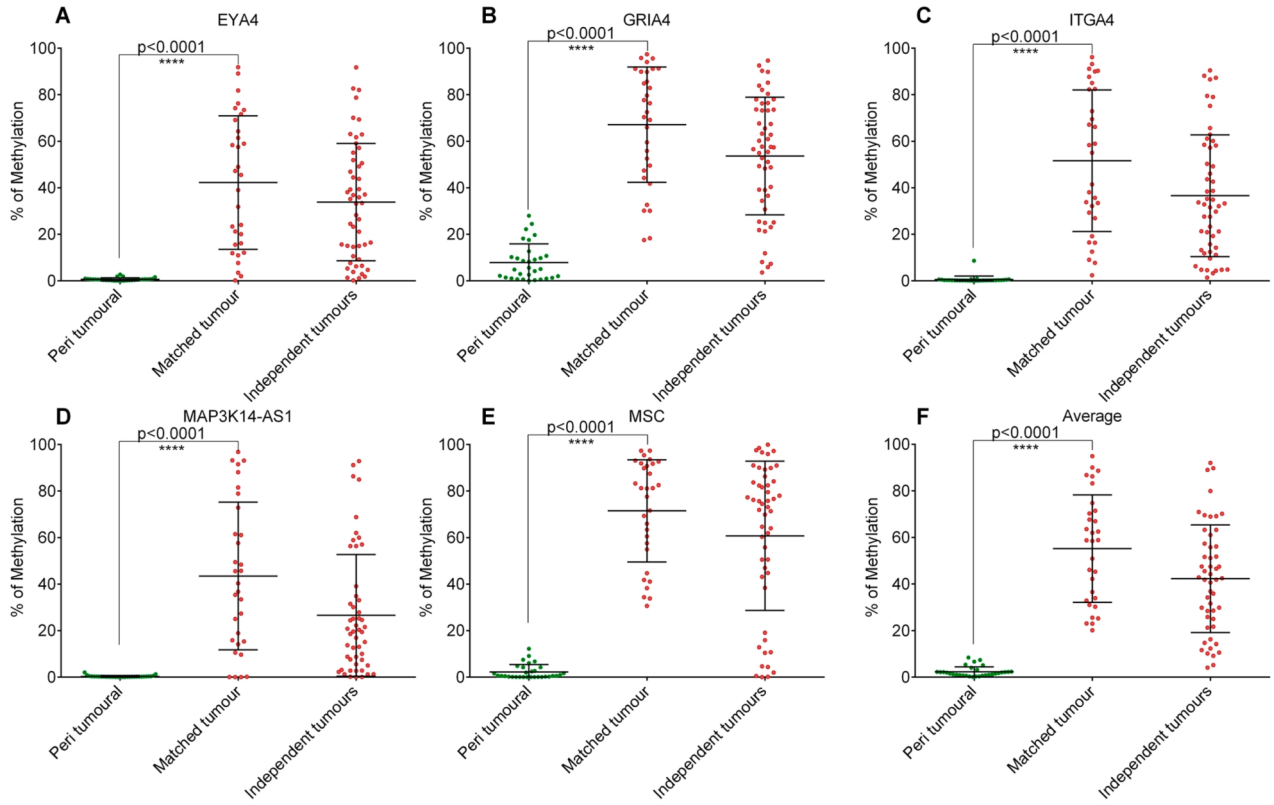

Figure 2 Prevalence of methylated markers in tissue DNA from patients with metastatic colorectal cancer (CRC). (A): *EYA4,* (B): *GRIA4,* (C): *ITGA4*, (D): *MAP3K14-AS1*, (E)*: MSC,* (F): average of the five markers. Samples from 82 patients with CRC were analysed. A first set was composed of 31 cases from which tumour and peritumoural tissue DNA were available. A second set of independent 51 tumour tissue specimens was assembled from remaining DNA extracted during the enrolment of two clinical trials.

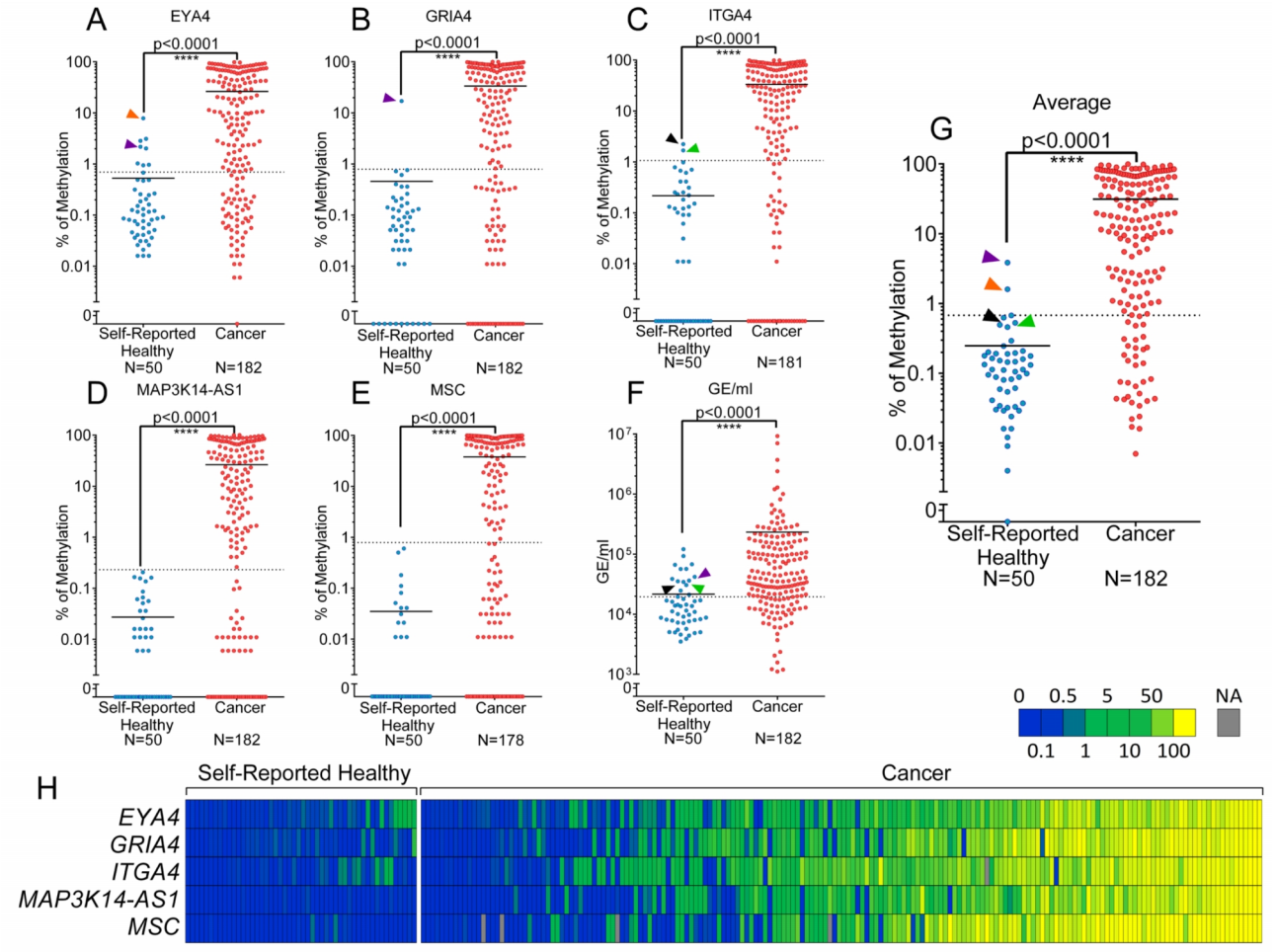

Figure 3 Prevalence of methylated markers in cell-free circulating DNA (cfDNA) and total amount of cfDNA. Plasma samples from 50 self-declared healthy donors (blue) and 182 patients with metastatic colorectal cancer (red) were analysed for the five selected markers. Group mean is represented by a horizontal bar. Mann-Whitney U test was performed to compare distribution in healthy patients and patients with cancer, which were all significantly different (with p<0.0001). Representation of individual markers: (A): *EYA4,* (B): *GRIA4,* (C): *ITGA4*, (D): *MAP3K14-AS1*, (E)*: MSC,* (F): genome equivalent/mL (GE/mL). (G): Representation of average methylation signal. Self-declared healthy donor plasma samples presenting more than one outlying value were indicated by coloured arrows; the dashed line corresponds to the threshold established by receiver operating characteristic curve (ROC) analyses available in online Supplementary file 7. (H): Heatmap of methylation values sorted by average methylation.

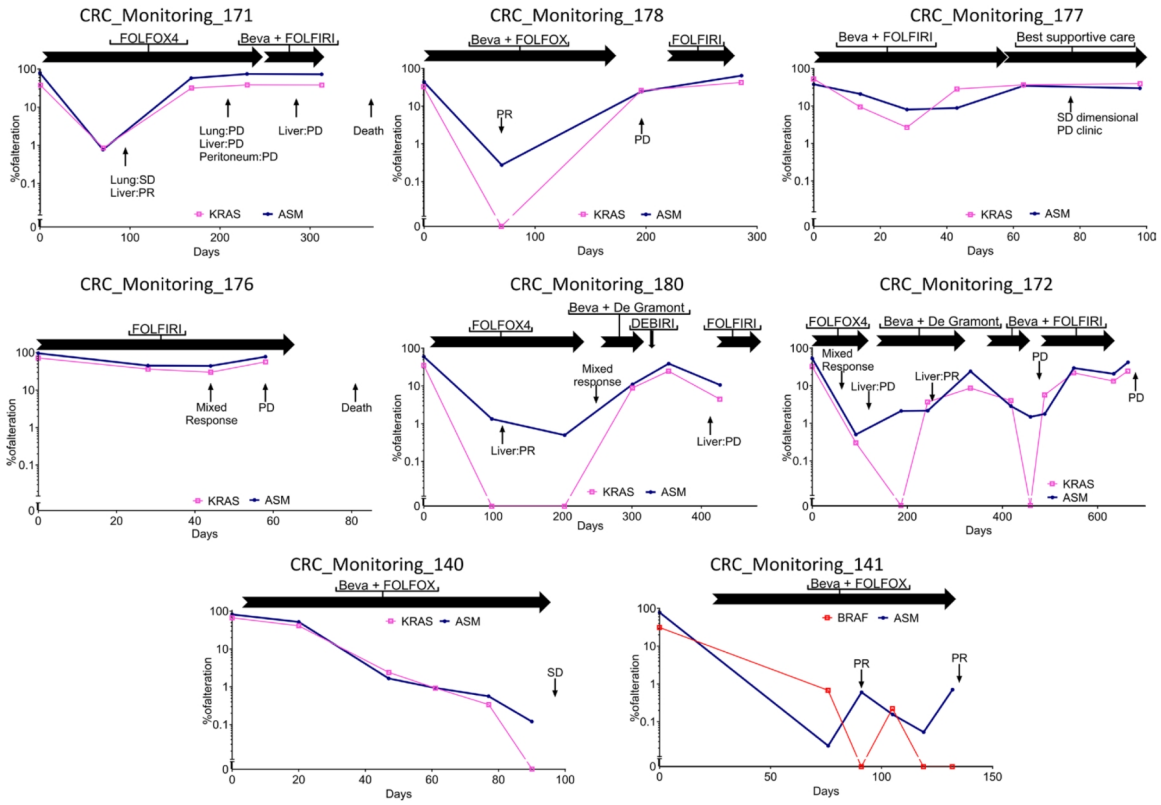

Figure 4 Average of selected markers (ASM) in cell-free circulating DNA dynamics in eight metastatic colorectal cancer (CRC) patients treated with conventional chemotherapy regimens. ASM is plotted in blue, while *KRAS* mutations are plotted in pink and *BRAF* in red. Methylation and genetic mutations evolve in parallel demonstrating the possibility to use methylation instead of genetic alterations for tracking response. Response status is indicated with arrows. PR, partial response; SD, stable disease; PD, progressive disease. Treatment periods are indicated as horizontal black arrows with corresponding chemotherapy regimens.

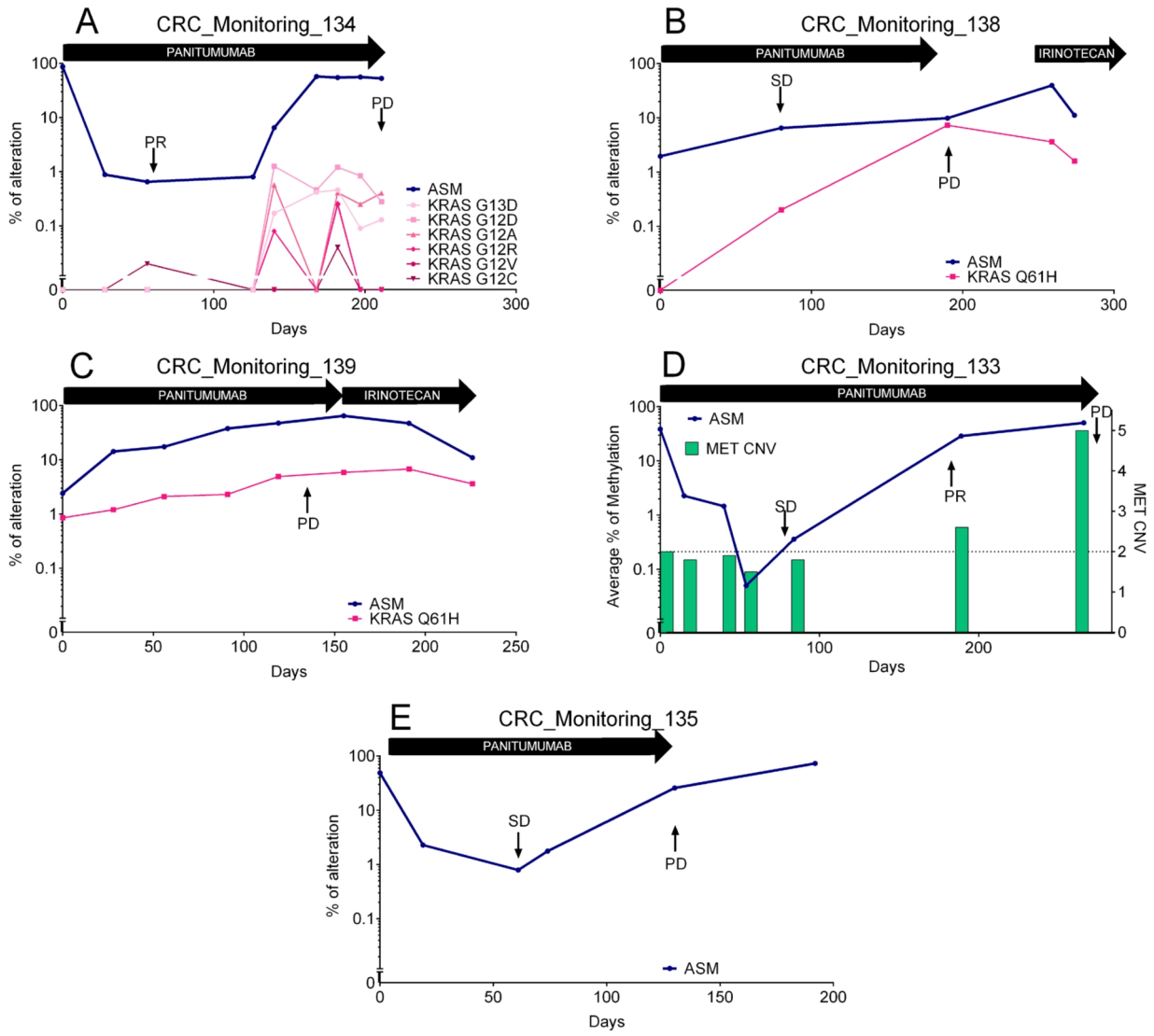

Figure 5 Average of selected markers (ASM) in cell-free circulating DNA dynamics in five metastatic colorectal cancer (CRC) patients treated with panitumumab for whom resistance causative mutations were discovered at progression and retrospectively assessed longitudinally. (A–C): Resistance was acquired through the emergence of a *KRAS* alteration; (D): resistance was acquired through the emergence of *MET* gene amplification. In each case, increase in ASM parallels the appearance of resistance alterations. (E): A case in which resistance mechanism remained unidentified but for which ASM could detect relapse.

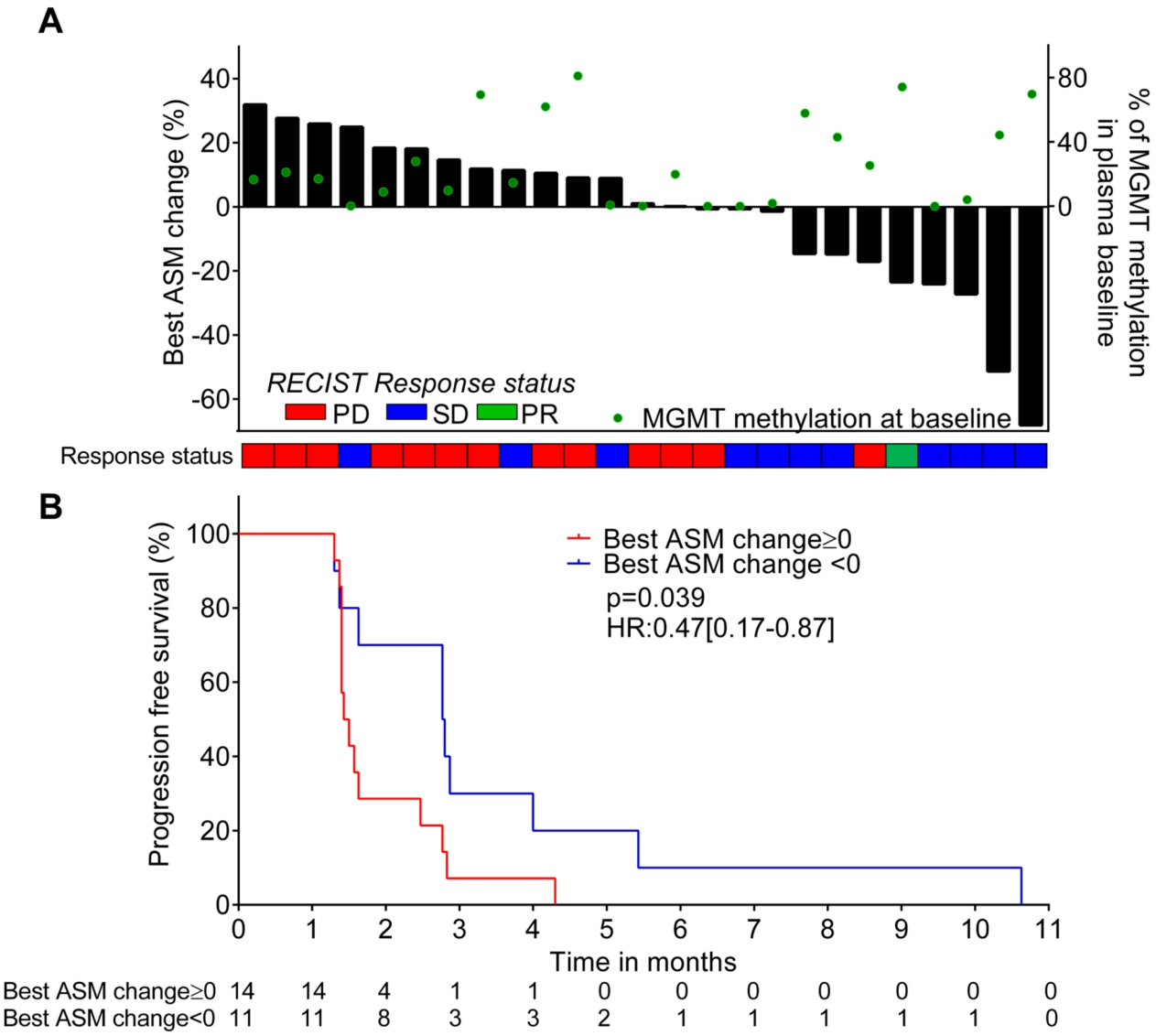

Figure 6 Average of selected markers (ASM) in cell-free circulating DNA dynamics assessment in patients with metastatic colorectal cancer treated with temozolomide within a clinical trial. (A): Comparison of ASM changes to response status evaluated by RECIST. The best ASM changes were plotted as a waterfall plot. Response status of patients evaluated by RECIST is plotted as a heatmap. (B): Progression-free survival according to best ASM change. Negative ASM change is associated with improved PFS. HR was estimated by log rank approach.

Supplementary File 1 - Supplementary Material and Methods

Cell lines and genome wide DNA methylation data processing and retrieval

A collection of 149 cell lines of intestinal origin (**Supplemental File 2A**) was assembled from different worldwide cell line banks or academic laboratories, as described previously [1].

DNA samples were extracted by Wizard SV Genomic DNA Purification System (Promega), and cell identity was confirmed using the Gene Print 10 System (Promega). DNA samples were checked for integrity by 1% agarose gel, and quantity via Picogreen quantification. All samples were bisulfite converted using the EZ DNA methylation Gold kit (Zymo Research) with a minimum input of 500 ng of gDNA following the manufacturer's instructions. Infinium HumanMethylation450 BeadChip arrays were carried out according to the Illumina Infinium HD methylation protocol. Raw methylation profiles have been deposited on Gene Expression Omnibus (GEO; http://www.ncbi.nlm.nih.gov/geo/; accession number: GSE86078).

GSE32146 was downloaded from GEO and considered as a control set (*i.e*. cancer unrelated normal mucosa, after removing the ulcerative colitis cases), for comparison with the cell lines. GSE41169 was downloaded from GEO and considered as a blood control (*i.e*. healthy donors) for verification of tissue specificity of the loci of interest.

GSE42752 [2] was downloaded from GEO and considered as a test cohort for the establishment of the beta-value threshold used for the *in-silico* validation. Level 1 data from the TCGA colorectal adenocarcinoma (COAD/READ) (http://cancergenome.nih.gov/; https://gdc.cancer.gov/) were downloaded and defined the validation cohort used for the *in-silico* validation. Further validation in normal tissues was performed GSE48684 [3]

Data Preprocessing and Marker Discovery Analysis

All raw data (IDAT files) were preprocessed in R Bioconductor using the minfi package [4] via the preprocessIllumina function (using background correction and control normalization) to achieve data normalized similarly to GEO downloaded datasets. The individual probe signal was removed when the detection p-value was above 0.05, and probes were removed from the dataset if more than 1% of the dataset contained no data. Our dataset was then merged with the other publically available cohorts before removal of probes containing SNPs [5], demonstrating sexual dimorphism [6] or located on sex chromosomes.

Differential probe analysis was performed using the lmFit function from limma package (choosing an adjusted p-value threshold of $1x10^{-35}$ and a minimum delta beta-value of 0.8). Probes were verified to not display any methylation in leukocytes (GSE41169; maximum beta-value allowed =0.1) insuring absence of false positivity in blood tests due to the high methylation value of blood cells. Differential region analysis was performed using the bumphunter function from the minfi package choosing a threshold of 0.8 and restricting the region to those represented by at least two probes ($L \geq 2$). Differentially methylated probes were limited to those overlapping differentially methylated regions, and “liquid biopsy” assessable loci were defined.

GSE42752 data were averaged for each of the genomic regions defined in the previous step according to sample type (normal and normal adjacent versus adenocarcinoma). Thresholds were calculated using Receiver operating characteristic analyses performed with the pROC package in R Bioconductor [7] considering normal and adjacent mucosa as positive outcome and cancer as negative; only loci showing a threshold below 0.35 were kept. Each characterized threshold were used to stratify the TCGA COREAD cohort, defining a positive predictive value (PPV) and negative predictive value (NPV) for discriminating normal adjacent from tumor tissue. Normal healthy and peri-tumoral

samples from GSE48684 [3] were also controlled for absence of methylation above the threshold.

Tissue collection and DNA isolation

Formalin fixed paraffin embedded tissues originated from two different cohorts. One containing macro-dissected tumor and normal adjacent tissues (N=31 cases; originating from several local hospitals) which were controlled for tumor purity and assembled at Niguarda Cancer Center, Grande Ospedale Metropolitano Niguarda (Milan, Italy) and from which DNA was newly extracted. A second cohort of independent tumor tissues (N=51) was assembled from remaining DNA extracted during the enrollement of the DETECT (EUDRACT 2011-002080-21) [33] or TEMECT (EUDRACT number 2012-003338-17) [34] trials.

Plasma Collection and DNA preparation

De-identified whole blood samples from healthy donors were purchased from the Brigham and Women's Hospital specimen bank (Boston, USA). Collection was performed in K2EDTA tubes between November 2009 and April 2010 from self-declared healthy donors aged 40 years and above who visited the hospital for an annual routine examination. The donors' sex and age was maintained in the datafile. Plasma was isolated after 10 minutes of centrifugation at 1600 RCF, and stored at -80°C.

One hundred and eighty two cases of mCRC were enrolled in the study. One hundred and thirty-seven cases were selected for plasma timepoints based on plasma sample availability at a time when patients were presenting radiological evidence of disease. The remaining 45 cases were treatment baselines, selected for availability of longitudinal

follow-up (additional total of 132 longitudinal samples). Summary of the clinico-pathological features of the two cohorts can be found in **Supplementary File 2D** (mCRC patients clinical features are presented in **Supplementary File 2E**). mCRC plasma samples were collected in K2EDTA tubes at Ospedale Niguarda Ca' Granda (Milan, Italy) between September 2009 and December 2015 or at Ospedale Molinette (Turin, Italy) between June 2013 to July 2015. Plasma was isolated in a two-step protocol (10 minutes at 1600 RCF, 10 minutes at 3000 RCF) and stored at -80°C until processing. The study was conducted according to Good Clinical Practices and was approved by the local ethics committee. One milliliter of plasma was processed for DNA extraction with the QIAamp Circulating Nucleic Acid Kit (Qiagen) or with the Maxwell® RSC ccfDNA Plasma Kit (Promega) following the manufacturer's protocol. Change in extraction kit (from Qiagen to Promega) was decided to improve the experimental throughput in a semi-automated fashion using the Maxwell® RSC ccfDNA Plasma Kit with no major change in extraction quality or yield. Twenty microliters of DNA were used for bisulfite conversion using the EZ DNA methylation Gold kit (Zymo Research), following the manufacturer's protocol, with final elution in 40 µl.

Methylation and genetic alteration assays for cfDNA evaluation

Selected loci were investigated for possible methylation independent amplification. Primers were designed using the PyroMark® Assay Design SW 2.0 (Qiagen) with custom settings. Primers and probes are available in **Supplemental Table 2C**. *In-silico* validation of the assays was performed using the same steps as previously described: threshold estimation in GSE42752 and stratification in TCGA COREAD, using solely the probes which were located within the amplicon **Supplementary File 5**. Optimization and evaluation of Methyl-BEAMing assays was performed as previously described [10], with the difference that beads were run on a BD C6 Accuri system (Becton-Dickinson). In-silico validation results display for the five markers of interest are available in **Supplementary File 4.**

Digital Miqe checklist including limit of detection, limit of blank, quantification ability (linearity and sensitivity) is available in **Supplementary File 3**.

Evaluation of genetic alterations (*KRAS*, *BRAF* mutations and *MET* gene copy number) in cfDNA was performed as previously described [11, 12]. Primers and probes are either commercially available (Biorad) or were custom designed and are listed in **Supplemental File 2C**.

References

1 Medico E, Russo M, Picco G, Cancelliere C, Valtorta E, Corti G, *et al.* The molecular landscape of colorectal cancer cell lines unveils clinically actionable kinase targets. Nature communications 2015;**6**:7002.

2 Naumov VA, Generozov EV, Zaharjevskaya NB, Matushkina DS, Larin AK, Chernyshov SV, *et al.* Genome-scale analysis of DNA methylation in colorectal cancer using Infinium HumanMethylation450 BeadChips. Epigenetics 2013;**8**:921-34.

3 Luo Y, Wong CJ, Kaz AM, Dzieciatkowski S, Carter KT, Morris SM, *et al.* Differences in DNA methylation signatures reveal multiple pathways of progression from adenoma to colorectal cancer. Gastroenterology 2014;**147**:418-29 e8.

4 Aryee MJ, Jaffe AE, Corrada-Bravo H, Ladd-Acosta C, Feinberg AP, Hansen KD, *et al.* Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. Bioinformatics 2014;**30**:1363-9.

5 Price ME, Cotton AM, Lam LL, Farre P, Emberly E, Brown CJ, *et al.* Additional annotation enhances potential for biologically-relevant analysis of the Illumina Infinium HumanMethylation450 BeadChip array. Epigenetics & chromatin 2013;**6**:4.

6 Chen YA, Lemire M, Choufani S, Butcher DT, Grafodatskaya D, Zanke BW, *et al.* Discovery of cross-reactive probes and polymorphic CpGs in the Illumina Infinium HumanMethylation450 microarray. Epigenetics 2013;**8**:203-9.

7 Robin X, Turck N, Hainard A, Tiberti N, Lisacek F, Sanchez JC, *et al.* pROC: an open-source package for R and S+ to analyze and compare ROC curves. BMC bioinformatics 2011;**12**:77.

8 Amatu A, Sartore-Bianchi A, Moutinho C, Belotti A, Bencardino K, Chirico G, *et al.* Promoter CpG island hypermethylation of the DNA repair enzyme MGMT predicts clinical response to dacarbazine in a phase II study for metastatic colorectal cancer. Clinical cancer research : an official journal of the American Association for Cancer Research 2013;**19**:2265-72.

9 Amatu A, Barault L, Moutinho C, Cassingena A, Bencardino K, Ghezzi S, *et al.* Tumor MGMT promoter hypermethylation changes over time limit temozolomide efficacy in a phase II trial for metastatic colorectal cancer. Annals of oncology : official journal of the European Society for Medical Oncology / ESMO 2016.

10 Barault L, Amatu A, Bleeker FE, Moutinho C, Falcomata C, Fiano V, *et al.* Digital PCR quantification of MGMT methylation refines prediction of clinical benefit from alkylating agents in glioblastoma and metastatic colorectal cancer. Annals of oncology : official journal of the European Society for Medical Oncology / ESMO 2015;**26**:1994-9.

11 Bardelli A, Corso S, Bertotti A, Hobor S, Valtorta E, Siravegna G, *et al.* Amplification of the MET receptor drives resistance to anti-EGFR therapies in colorectal cancer. Cancer discovery 2013;**3**:658-73.

12 Siravegna G, Mussolin B, Buscarino M, Corti G, Cassingena A, Crisafulli G, *et al.* Clonal evolution and resistance to EGFR blockade in the blood of colorectal cancer patients. Nature medicine 2015;**21**:827.

Supplementary File 2A

List of samples used in the marker discovery analysis

SAMPLES USED FOR THE MARKER DISCOVERY

Sample_Name	Tissue_type	Donor_type	Dataset	Sentrix_ID	Sentrix_Position	Official_name
C10	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998998097	R02C02	C10
C106	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455219	R03C02	C106
C125PM	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999875059	R06C02	C125PM
C146	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999876007	R02C01	C146
C170	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455225	R05C01	C170
C32	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426028	R06C01	C32
C70	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426028	R06C02	C70
C75	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647450147	R05C02	C75
C80	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455207	R01C01	C80
C84	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455254	R05C02	C84
C99	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999002152	R06C01	C99
CACO2	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426003	R06C01	CACO-2
CaR1	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200486890054	R06C01	CAR-1
CCK81	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999002152	R02C01	CCK81
CL11	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426028	R01C02	CL-11
CL14	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455235	R06C01	CL-14
CL34	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999875081	R01C02	CL-34
CL40	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455254	R02C01	CL-40
Co115	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455235	R05C01	Co-115
COCM1	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999002152	R04C02	COCM-1
COGA1	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10011071041	R01C01	COGA-1
COGA12	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455255	R06C01	COGA-12
COGA2	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10011071041	R02C02	COGA-2
COGA3	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10011071041	R03C02	COGA-3
COGA5	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999875059	R01C01	COGA-5
COGA5L	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455197	R01C02	COGA-5L
COGA8	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999875129	R03C02	COGA-8
COLO201	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10011071041	R04C01	COLO-201
COLO205	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200486890054	R01C02	COLO-205
COLO320DM	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10011071041	R06C02	COLO-320DM
COLO320HSR	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200486890054	R02C02	COLO-320HSR
COLO60H	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999875129	R06C01	COLO-60H
COLO678	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426028	R01C01	COLO-678
COLO94H	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455197	R01C01	COLO-94H
CX1	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999875081	R03C01	CX1
DiFi	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10011071041	R05C02	DiFi
DLD1	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200486890054	R03C02	DLD1
FET	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999002152	R05C02	FET
GEO	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455251	R04C01	GEO
GP2d	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455255	R05C02	GP2d
Gp5D	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590020	R01C01	Gp5d
HCA24	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455172	R02C01	HCA24
HCA46	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998998097	R02C01	HCA46
HCA7	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455255	R04C02	HCA7
HCC2998	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426003	R05C02	HCC2998
HCT116	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200486890054	R04C02	HCT-116
HCT15	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200486890054	R05C02	HCT-15
HCT8	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10011071041	R06C01	HCT-8
HDC114	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455164	R05C01	HDC114
HDC135	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455255	R03C01	HDC135
HDC142	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10006823050	R02C01	HDC142
HDC143	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999875089	R06C01	HDC143
HDC54	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455235	R03C02	HDC54
HDC8	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455199	R03C01	HDC8
HDC82	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455172	R06C02	HDC82
HDC9	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455199	R02C01	HDC9
HRA16	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647450147	R06C02	HRA16
HROC18	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10006823050	R04C02	HROC18
HROC24	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455172	R02C02	HROC24
HROC32	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998998097	R05C02	HROC32
HROC39	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455255	R02C01	HROC39
HROC46	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455235	R01C01	HROC46
HROC69	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455251	R04C02	HROC69
HROC80	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455219	R06C01	HROC80
HROC87	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647450134	R05C01	HROC87
HT115	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200486890054	R06C02	HT-115
HT29	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590019	R01C01	HT-29
HT55	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590020	R02C01	HT-55
HUTU80	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590019	R02C01	HuTu80
KM12	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590020	R03C01	KM-12
KM12C	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455172	R03C01	KM-12C
KM12SM	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999875089	R05C01	KM-12SM
KM20	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999875081	R06C01	KM-20
LIM1215	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10011071041	R02C01	LIM-1215
LIM1899	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647450134	R04C01	LIM-1899
LIM2099	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998998097	R06C01	LIM-2099
LIM2405	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455199	R02C02	LIM-2405
LIM2412	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647450134	R02C01	LIM-2412
LIM2537	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455251	R05C02	LIM-2537
LIM2550	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455172	R05C02	LIM-2550
LIM2551	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455172	R01C01	LIM-2551
LoVo	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426003	R03C02	LoVo
LS1034	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426003	R06C02	LS1034
LS123	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590020	R04C01	LS123
LS174T	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998998097	R06C02	LS174T
LS180	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590019	R03C01	LS180
LS411N	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426003	R03C01	LS411N
LS513	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590020	R02C02	LS513
MDST8	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590019	R04C01	MDST8
MIP101	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10006823050	R01C02	MIP101
NCIH498	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999875081	R04C01	NCI-H498
NCIH508	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10006823050	R05C01	NCI-H508

NCIH630	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590020	R05C01	NCI-H630
NCIH684	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455255	R01C02	NCI-H684
NCIH716	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590019	R05C01	NCI-H716
NCIH747	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590019	R06C01	NCI-H747
OUMS23	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455199	R01C01	OUMS-23
OXCO1	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455235	R01C02	OXCO1
OXCO2	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10006823050	R03C02	OXCO2
OXCO3	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999875118	R03C01	OXCO3
RCM1	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590019	R01C02	RCM1
RKO	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426003	R01C01	RKO
RW7213	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455123	R04C01	RW7213
SKCO1	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426028	R02C02	SKCO-1
SNU1033	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455172	R01C02	SNU-1033
SNU1040	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426028	R04C02	SNU-1040
SNU1047	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426028	R02C01	SNU-1047
SNU1181	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999875118	R04C01	SNU-1181
SNU1235	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647450147	R04C01	SNU-1235
SNU1406	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10006823050	R04C01	SNU-1406
SNU1411	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647450147	R05C01	SNU-1411
SNU1460	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10006823050	R06C02	SNU-1460
SNU1544	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10006823050	R06C01	SNU-1544
SNU1684	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455225	R04C01	SNU-1684
SNU1746	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455225	R03C02	SNU-1746
SNU175	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426028	R05C02	SNU-175
SNU254	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455254	R03C02	SNU-254
SNU283	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426003	R04C01	SNU-283
SNU407	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426003	R01C02	SNU-407
SNU479	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455123	R04C02	SNU-479
SNU503	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999875089	R02C02	SNU-503
SNU61	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426003	R02C01	SNU-61
SNU769B	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998998097	R03C01	SNU-769B
SNU81	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455164	R01C01	SNU-81
SNU977	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998998097	R03C02	SNU-977
SNUC1	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426003	R05C01	SNU-C1
SNUC2A	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455164	R01C02	SNU-C2A
SNUC2B	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590019	R02C02	SNU-C2B
SNUC4	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999876007	R04C01	SNU-C4
SNUC5	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426003	R02C02	SNU-C5
SW1116	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590019	R03C02	SW1116
SW1222	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647450134	R06C01	SW1222
SW1417	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426028	R05C01	SW1417
SW1463	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590019	R04C02	SW1463
SW403	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	10006823050	R03C01	SW403
SW48	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	6042324140	R02C01	SW48
SW480	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590019	R05C02	SW480
SW620	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590019	R06C02	SW620
SW837	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426003	R04C02	SW-837
SW948	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590020	R06C01	SW-948
T84	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	200693590020	R01C02	T84
V411	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455207	R03C02	V411
V457	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999002152	R03C02	V457
V481	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455251	R02C01	V481
V703	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999002152	R04C01	V703
VACO432	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426028	R03C01	VACO-432
VACO5	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3999875081	R06C02	VACO-5
VACO6	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	9647455255	R01C01	VACO-6
WiDR	Cell_line	Colon_Adenocarcinoma_cell	GSE86078	3998426028	R04C01	WiDR

PUBLICALLY AVAILABLE DATA USED IN THE STUDY

Sample_Name	Tissue_type	Donor_type	Dataset	Sentrix_ID	Sentrix_Position
GSM796576	Normal_mucosa	Healthy	GSE32146		
GSM796577	Normal_mucosa	Healthy	GSE32146		
GSM796578	Normal_mucosa	Healthy	GSE32146		
GSM796579	Normal_mucosa	Healthy	GSE32146		
GSM796580	Normal_mucosa	Healthy	GSE32146		
GSM796581	Normal_mucosa	Healthy	GSE32146		
GSM796582	Normal_mucosa	Healthy	GSE32146		
GSM796583	Normal_mucosa	Healthy	GSE32146		
GSM796584	Normal_mucosa	Healthy	GSE32146		
GSM796585	Normal_mucosa	Healthy	GSE32146		
GSM796586	Normal_mucosa	Crohn's_disease	GSE32146		
GSM796587	Normal_mucosa	Crohn's_disease	GSE32146		
GSM796588	Normal_mucosa	Crohn's_disease	GSE32146		
GSM796589	Normal_mucosa	Crohn's_disease	GSE32146		
GSM796590	Normal_mucosa	Crohn's_disease	GSE32146		
GSM796591	Normal_mucosa	Crohn's_disease	GSE32146		
GSM796592	Normal_mucosa	Crohn's_disease	GSE32146		
GSM796593	Normal_mucosa	Crohn's_disease	GSE32146		
GSM796594	Normal_mucosa	Crohn's_disease	GSE32146		
GSM796598	Normal_mucosa	Crohn's_disease	GSE32146		
GSM1009660	Whole_Blood	Healthy_Blood	GSE41169		
GSM1009666	Whole_Blood	Healthy_Blood	GSE41169		
GSM1009667	Whole_Blood	Healthy_Blood	GSE41169		
GSM1009668	Whole_Blood	Healthy_Blood	GSE41169		
GSM1009673	Whole_Blood	Healthy_Blood	GSE41169		
GSM1009674	Whole_Blood	Healthy_Blood	GSE41169		
GSM1009677	Whole_Blood	Healthy_Blood	GSE41169		
GSM1009681	Whole_Blood	Healthy_Blood	GSE41169		
GSM1009685	Whole_Blood	Healthy_Blood	GSE41169		
GSM1009686	Whole_Blood	Healthy_Blood	GSE41169		
GSM1009687	Whole_Blood	Healthy_Blood	GSE41169		
GSM1009688	Whole_Blood	Healthy_Blood	GSE41169		
GSM1009689	Whole_Blood	Healthy_Blood	GSE41169		
GSM1009690	Whole_Blood	Healthy_Blood	GSE41169		

GSM1009691	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009692	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009693	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009694	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009695	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009697	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009723	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009727	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009729	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009739	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009742	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009743	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009744	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009745	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009746	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009747	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009748	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009749	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009892	Whole_Blood	Healthy_Blood	GSE41169	
GSM1009893	Whole_Blood	Healthy_Blood	GSE41169	
GSM1049367	Normal_mucosa	Healthy	GSE42752	
GSM1049368	Normal_mucosa	Healthy	GSE42752	
GSM1049369	Normal_mucosa	Healthy	GSE42752	
GSM1049370	Normal_mucosa	Healthy	GSE42752	
GSM1049371	Normal_mucosa	Healthy	GSE42752	
GSM1049372	Normal_mucosa	Healthy	GSE42752	
GSM1049373	Normal_mucosa	Healthy	GSE42752	
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GSM1049380	Normal_mucosa	Healthy	GSE42752	
GSM1049381	Normal_mucosa	Healthy	GSE42752	
GSM1049382	Normal_mucosa	Healthy	GSE42752	
GSM1049383	Normal_mucosa	Healthy	GSE42752	
GSM1049384	Normal_mucosa	Healthy	GSE42752	
GSM1049385	Normal_mucosa	Healthy	GSE42752	
GSM1049386	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049387	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049388	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049389	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049390	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049391	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049392	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049393	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049394	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049395	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049396	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049397	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049398	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
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GSM1049401	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049402	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049403	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049404	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049405	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049406	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049407	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE42752	
GSM1049408	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049409	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049410	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049411	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049412	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049413	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049414	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049415	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049416	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049417	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049418	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049419	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049420	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049421	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049422	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049423	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049424	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049425	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049426	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049427	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049428	Tumor	Colon_Adenocarcinoma	GSE42752	
GSM1049429	Tumor	Colon_Adenocarcinoma	GSE42752	
TCGA-A6-2671-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041068 R01C02
TCGA-A6-2675-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6042316001 R03C01
TCGA-A6-2679-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041068 R04C01
TCGA-A6-2680-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041068 R06C01
TCGA-A6-2681-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041068 R02C02
TCGA-A6-2682-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041068 R03C02
TCGA-A6-2684-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041068 R01C01
TCGA-A6-2685-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041068 R02C01
TCGA-A6-2686-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041068 R03C01
TCGA-A6-4107-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041068 R05C01
TCGA-A6-5667-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6042316015 R05C01
TCGA-AA-3488-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041088 R04C01
TCGA-AA-3492-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041084 R05C02

TCGA-AA-3494-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041065 R02C02
TCGA-AA-3495-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041088 R02C02
TCGA-AA-3502-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041065 R04C02
TCGA-AA-3506-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041007 R01C02
TCGA-AA-3509-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041084 R06C02
TCGA-AA-3510-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	5775041084 R03C02
TCGA-AA-3655-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6042316015 R06C02
TCGA-AA-3660-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6042308165 R05C01
TCGA-AA-3663-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6042316001 R05C02
TCGA-AA-3697-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6042308165 R04C02
TCGA-AA-3712-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6042316011 R03C01
TCGA-AA-3713-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6042308165 R04C01
TCGA-AG-3725-11	Normal_mucosa	Rectal_Adenocarcinoma_norm	TCGA COREAD	6055424097 R02C02
TCGA-AG-3731-11	Normal_mucosa	Rectal_Adenocarcinoma_norm	TCGA COREAD	6055424075 R04C01
TCGA-AG-A01W-11	Normal_mucosa	Rectal_Adenocarcinoma_norm	TCGA COREAD	5775041086 R02C01
TCGA-AG-A01Y-11	Normal_mucosa	Rectal_Adenocarcinoma_norm	TCGA COREAD	5775041086 R05C01
TCGA-AG-A020-11	Normal_mucosa	Rectal_Mucinous_Adenocarcinoma_norm	TCGA COREAD	5775041086 R01C02
TCGA-AG-A02N-11	Normal_mucosa	Rectal_Adenocarcinoma_norm	TCGA COREAD	5775041086 R04C02
TCGA-AG-A036-11	Normal_mucosa	Rectal_Adenocarcinoma_norm	TCGA COREAD	5775041086 R06C02
TCGA-AZ-6598-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6057825035 R06C02
TCGA-AZ-6599-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6057825028 R03C02
TCGA-AZ-6600-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6057825020 R04C01
TCGA-AZ-6601-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6057825002 R01C02
TCGA-G4-6295-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6042308165 R06C02
TCGA-G4-6297-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6042316015 R05C02
TCGA-G4-6298-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6042308159 R02C01
TCGA-G4-6302-11	Normal_mucosa	Colon_Mucinous_Adenocarcinoma_norm	TCGA COREAD	6042316001 R02C01
TCGA-G4-6311-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6042308159 R02C02
TCGA-G4-6314-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6042316015 R01C02
TCGA-G4-6320-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6042308165 R02C01
TCGA-G4-6322-11	Normal_mucosa	Colon_Mucinous_Adenocarcinoma_norm	TCGA COREAD	6042308159 R01C01
TCGA-G4-6625-11	Normal_mucosa	Colon_Adenocarcinoma_norm	TCGA COREAD	6057825028 R04C02
TCGA-3L-AA1B-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9702496157 R02C02
TCGA-4N-A93T-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9702496157 R06C01
TCGA-4T-AA8H-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	3999492120 R06C01
TCGA-5M-AAT4-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	3999492115 R06C02
TCGA-5M-AAT5-01	Tumor	NA	TCGA COREAD	3999492120 R05C01
TCGA-5M-AAT6-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	3999492120 R02C02
TCGA-5M-AATA-01	Tumor	NA	TCGA COREAD	3999492115 R05C02
TCGA-5M-AATE-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	3999492120 R06C02
TCGA-A6-2671-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041065 R01C02
TCGA-A6-2675-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316015 R04C01
TCGA-A6-2677-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9305216012 R01C02
TCGA-A6-2677-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9305216012 R02C02
TCGA-A6-2679-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041065 R04C01
TCGA-A6-2680-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041084 R01C01
TCGA-A6-2681-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041088 R03C02
TCGA-A6-2682-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041084 R06C01
TCGA-A6-2684-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041007 R02C01
TCGA-A6-2684-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9305216012 R03C02
TCGA-A6-2684-01-3	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9305216012 R04C02
TCGA-A6-2685-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041088 R06C01
TCGA-A6-2686-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041007 R04C01
TCGA-A6-3809-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	9305216012 R05C02
TCGA-A6-3809-01-2	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	9305216012 R06C02
TCGA-A6-3810-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9305216015 R01C01
TCGA-A6-3810-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9305216015 R02C01
TCGA-A6-4105-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825020 R03C02
TCGA-A6-4107-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041065 R01C01
TCGA-A6-5656-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718065 R06C01
TCGA-A6-5656-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9305216015 R03C01
TCGA-A6-5656-01-3	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9305216015 R04C01
TCGA-A6-5657-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625037 R04C02
TCGA-A6-5659-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625037 R01C01
TCGA-A6-5659-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9305216015 R05C01
TCGA-A6-5659-01-3	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9305216015 R06C01
TCGA-A6-5660-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625037 R01C02
TCGA-A6-5661-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625011 R06C01
TCGA-A6-5661-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	7796806109 R05C02
TCGA-A6-5662-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625011 R01C01
TCGA-A6-5664-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718079 R04C02
TCGA-A6-5665-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625057 R02C02
TCGA-A6-5665-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	7796806109 R03C02
TCGA-A6-5666-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625057 R01C02
TCGA-A6-5667-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316015 R03C02
TCGA-A6-6137-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825028 R01C01
TCGA-A6-6138-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825020 R01C02
TCGA-A6-6140-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825002 R03C02
TCGA-A6-6141-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825020 R02C01
TCGA-A6-6142-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825028 R01C02
TCGA-A6-6648-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825020 R03C01
TCGA-A6-6649-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825020 R06C02
TCGA-A6-6650-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825028 R05C02
TCGA-A6-6650-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9305216015 R01C02
TCGA-A6-6650-01-3	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9305216015 R02C02
TCGA-A6-6651-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718053 R05C01
TCGA-A6-6652-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825028 R06C01
TCGA-A6-6653-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825028 R06C02
TCGA-A6-6654-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718065 R02C01
TCGA-A6-6780-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6929718053 R04C01
TCGA-A6-6780-01-2	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	9305216015 R03C02
TCGA-A6-6780-01-3	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	9305216015 R04C02
TCGA-A6-6781-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6264509018 R01C01
TCGA-A6-6781-01-2	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6264509087 R05C02
TCGA-A6-6781-01-3	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	9305216015 R05C02
TCGA-A6-6781-01-4	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	9305216015 R06C02
TCGA-A6-6782-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718053 R03C02

TCGA-A6-A565-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	9296931074	R02C01
TCGA-A6-A566-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	9296931073	R05C01
TCGA-A6-A567-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9296931074	R04C01
TCGA-A6-A56B-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9296931073	R04C01
TCGA-A6-A5ZU-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9296931073	R03C02
TCGA-AA-3488-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041084	R04C01
TCGA-AA-3489-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718053	R06C02
TCGA-AA-3492-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041065	R06C01
TCGA-AA-3494-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041088	R01C01
TCGA-AA-3495-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041007	R01C01
TCGA-AA-3496-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718065	R06C02
TCGA-AA-3502-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041088	R06C02
TCGA-AA-3506-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041065	R03C02
TCGA-AA-3509-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041088	R04C02
TCGA-AA-3510-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041065	R02C01
TCGA-AA-3511-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718065	R05C01
TCGA-AA-3655-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308165	R01C01
TCGA-AA-3660-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308158	R06C02
TCGA-AA-3662-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308159	R05C02
TCGA-AA-3663-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316001	R04C02
TCGA-AA-3697-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316015	R02C02
TCGA-AA-3712-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308165	R02C02
TCGA-AA-3713-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316001	R01C01
TCGA-AD-5900-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6285625011	R02C02
TCGA-AD-6548-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718054	R05C01
TCGA-AD-6888-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509018	R05C01
TCGA-AD-6888-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509087	R03C02
TCGA-AD-6889-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509018	R03C02
TCGA-AD-6889-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509087	R04C02
TCGA-AD-6890-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509018	R02C02
TCGA-AD-6890-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509087	R01C01
TCGA-AD-6895-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509087	R05C01
TCGA-AD-6899-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6264509087	R01C02
TCGA-AD-6901-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264496026	R06C02
TCGA-AD-6963-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509087	R03C01
TCGA-AD-6963-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509127	R03C01
TCGA-AD-6964-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509018	R02C01
TCGA-AD-6964-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509087	R06C02
TCGA-AD-6965-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509018	R05C02
TCGA-AD-6965-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509018	R06C01
TCGA-AD-A5EJ-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9296931073	R06C01
TCGA-AD-A5EK-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9296931073	R02C02
TCGA-AF-2687-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424097	R04C02
TCGA-AF-2690-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424097	R01C02
TCGA-AF-2693-01	Tumor	NA	TCGA COREAD	6055424075	R04C02
TCGA-AF-3911-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424097	R05C02
TCGA-AF-4110-01	Tumor	NA	TCGA COREAD	6055424097	R04C01
TCGA-AF-6136-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718081	R03C01
TCGA-AF-6655-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718081	R02C01
TCGA-AF-6672-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718081	R06C02
TCGA-AF-A56K-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	9828653044	R03C02
TCGA-AF-A56L-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	9828653044	R04C02
TCGA-AF-A56N-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	9828653044	R05C02
TCGA-AG-3591-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424075	R03C01
TCGA-AG-3592-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424075	R03C02
TCGA-AG-3725-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424075	R01C01
TCGA-AG-3731-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424040	R04C02
TCGA-AG-3732-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718058	R01C01
TCGA-AG-3742-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718058	R02C02
TCGA-AG-4021-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424097	R03C02
TCGA-AG-4022-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424097	R06C02
TCGA-AG-A01W-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	5775041086	R01C01
TCGA-AG-A01Y-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	5775041086	R04C01
TCGA-AG-A020-01	Tumor	Rectal_Mucinous_Adenocarcinoma	TCGA COREAD	5775041086	R06C01
TCGA-AG-A026-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	5775041086	R02C02
TCGA-AG-A02N-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	5775041086	R03C02
TCGA-AG-A036-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	5775041086	R05C02
TCGA-AH-6544-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718058	R06C02
TCGA-AH-6547-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718061	R05C02
TCGA-AH-6549-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718081	R05C01
TCGA-AH-6643-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718061	R06C02
TCGA-AH-6644-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718081	R04C02
TCGA-AH-6897-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718114	R05C01
TCGA-AH-6903-01	Tumor	Rectal_Mucinous_Adenocarcinoma	TCGA COREAD	6929718114	R02C01
TCGA-AM-5820-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625037	R03C02
TCGA-AM-5821-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625037	R02C01
TCGA-AU-3779-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316001	R04C01
TCGA-AU-6004-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308159	R01C02
TCGA-AY-5543-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625037	R06C02
TCGA-AY-6196-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6042308165	R06C01
TCGA-AY-6197-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308159	R06C02
TCGA-AY-6386-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308165	R01C02
TCGA-AY-A54L-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9296931073	R01C02
TCGA-AY-A69D-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9702496157	R05C01
TCGA-AY-A71X-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	9702496157	R03C02
TCGA-AY-A8YK-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	3999492120	R03C01
TCGA-AZ-4308-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041065	R03C01
TCGA-AZ-4313-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041065	R05C02
TCGA-AZ-4315-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041084	R02C02
TCGA-AZ-4323-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718079	R06C01
TCGA-AZ-4614-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041084	R01C02
TCGA-AZ-4615-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041007	R03C01
TCGA-AZ-4616-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718054	R03C01
TCGA-AZ-4681-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041088	R01C02
TCGA-AZ-4682-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041065	R05C01
TCGA-AZ-4684-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041088	R05C02
TCGA-AZ-5403-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625057	R02C01
TCGA-AZ-5407-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308158	R04C02

TCGA-AZ-6598-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825020 R04C02
TCGA-AZ-6599-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825020 R05C01
TCGA-AZ-6600-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825020 R02C02
TCGA-AZ-6601-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825002 R05C01
TCGA-AZ-6603-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718053 R01C02
TCGA-AZ-6605-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718054 R01C02
TCGA-AZ-6606-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718065 R01C02
TCGA-AZ-6607-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718079 R03C02
TCGA-AZ-6608-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718065 R05C02
TCGA-BM-6198-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424075 R01C02
TCGA-CA-5254-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718065 R01C01
TCGA-CA-5255-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718053 R04C02
TCGA-CA-5256-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041084 R05C01
TCGA-CA-5796-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6285625037 R05C01
TCGA-CA-5797-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625057 R06C01
TCGA-CA-6715-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718054 R05C02
TCGA-CA-6716-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718054 R02C01
TCGA-CA-6717-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6929718079 R05C01
TCGA-CA-6718-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718054 R01C01
TCGA-CA-6719-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718079 R01C02
TCGA-CI-6619-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718081 R01C01
TCGA-CI-6620-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718058 R03C02
TCGA-CI-6621-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718061 R01C01
TCGA-CI-6622-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718061 R06C01
TCGA-CI-6623-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718061 R01C02
TCGA-CI-6624-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718058 R04C02
TCGA-CK-4947-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625037 R04C01
TCGA-CK-4948-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625068 R06C01
TCGA-CK-4950-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308165 R03C01
TCGA-CK-4951-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	5775041084 R04C02
TCGA-CK-4952-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6042308158 R03C01
TCGA-CK-5912-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625057 R01C01
TCGA-CK-5913-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625057 R05C01
TCGA-CK-5914-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625011 R05C02
TCGA-CK-5915-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625011 R01C02
TCGA-CK-5916-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625037 R02C02
TCGA-CK-6746-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718079 R02C02
TCGA-CK-6747-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718053 R03C01
TCGA-CK-6748-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6929718079 R04C01
TCGA-CK-6751-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6929718054 R06C01
TCGA-CL-4957-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424040 R03C02
TCGA-CL-5917-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718042 R01C02
TCGA-CL-5918-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718058 R05C01
TCGA-CM-4743-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316001 R06C02
TCGA-CM-4744-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041065 R06C02
TCGA-CM-4746-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041007 R05C01
TCGA-CM-4747-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041088 R02C01
TCGA-CM-4748-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	5775041084 R03C01
TCGA-CM-4750-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041007 R06C01
TCGA-CM-4751-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718053 R02C02
TCGA-CM-4752-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041088 R03C01
TCGA-CM-5341-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	5775041088 R05C01
TCGA-CM-5344-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316001 R06C01
TCGA-CM-5348-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316015 R06C01
TCGA-CM-5349-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316011 R06C01
TCGA-CM-5860-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625037 R05C02
TCGA-CM-5861-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625011 R04C01
TCGA-CM-5862-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625068 R04C01
TCGA-CM-5863-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6929718053 R01C01
TCGA-CM-5864-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625068 R05C01
TCGA-CM-5868-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625057 R04C01
TCGA-CM-6161-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625037 R06C01
TCGA-CM-6162-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6285625068 R01C02
TCGA-CM-6163-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929671148 R03C01
TCGA-CM-6164-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625068 R03C01
TCGA-CM-6165-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929671148 R06C01
TCGA-CM-6166-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625011 R05C01
TCGA-CM-6167-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929671148 R05C01
TCGA-CM-6168-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929671148 R04C01
TCGA-CM-6169-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625057 R04C02
TCGA-CM-6170-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625057 R03C01
TCGA-CM-6171-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625037 R03C01
TCGA-CM-6172-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625068 R01C01
TCGA-CM-6674-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718054 R03C02
TCGA-CM-6675-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718054 R04C01
TCGA-CM-6676-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718053 R02C01
TCGA-CM-6677-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718065 R04C01
TCGA-CM-6678-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718054 R04C02
TCGA-CM-6679-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718079 R05C02
TCGA-CM-6680-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718054 R06C02
TCGA-D5-5537-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509018 R04C02
TCGA-D5-5537-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509127 R02C01
TCGA-D5-5538-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929671148 R02C01
TCGA-D5-5539-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6285625011 R04C02
TCGA-D5-5540-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625011 R03C01
TCGA-D5-5541-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625011 R02C01
TCGA-D5-6529-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825028 R04C01
TCGA-D5-6530-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316011 R04C01
TCGA-D5-6531-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308158 R05C02
TCGA-D5-6532-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308165 R03C02
TCGA-D5-6533-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308158 R02C01
TCGA-D5-6534-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6264509087 R02C01
TCGA-D5-6534-01-2	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6264509127 R05C01
TCGA-D5-6535-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316011 R01C01
TCGA-D5-6536-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308159 R04C01
TCGA-D5-6537-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308158 R03C02
TCGA-D5-6538-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316015 R01C01
TCGA-D5-6539-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316011 R05C01

TCGA-D5-6540-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6042316001 R01C02
TCGA-D5-6541-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308158 R01C01
TCGA-D5-6898-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509087 R04C01
TCGA-D5-6898-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509087 R06C01
TCGA-D5-6922-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509127 R01C01
TCGA-D5-6923-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509127 R04C01
TCGA-D5-6924-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509018 R03C01
TCGA-D5-6924-01-2	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509018 R06C02
TCGA-D5-6926-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509018 R01C02
TCGA-D5-6930-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6264509087 R02C02
TCGA-D5-7000-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6264509018 R04C01
TCGA-DC-4745-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424040 R06C01
TCGA-DC-4749-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424040 R06C02
TCGA-DC-5337-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718042 R06C01
TCGA-DC-5869-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718058 R06C01
TCGA-DC-6154-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718113 R03C02
TCGA-DC-6155-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718042 R03C02
TCGA-DC-6156-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718042 R02C02
TCGA-DC-6157-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718058 R02C01
TCGA-DC-6158-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718042 R04C02
TCGA-DC-6160-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718058 R01C02
TCGA-DC-6681-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718081 R03C02
TCGA-DC-6682-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718081 R01C02
TCGA-DC-6683-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718081 R05C02
TCGA-DM-A0X9-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316010 R04C02
TCGA-DM-A0XD-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316010 R06C02
TCGA-DM-A0XF-01	Tumor	NA	TCGA COREAD	6042316008 R02C01
TCGA-DM-A1D0-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316008 R04C01
TCGA-DM-A1D4-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316008 R06C01
TCGA-DM-A1D6-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6042316008 R02C02
TCGA-DM-A1D7-01	Tumor	NA	TCGA COREAD	6042316008 R03C02
TCGA-DM-A1D8-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316010 R05C02
TCGA-DM-A1D9-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316008 R01C01
TCGA-DM-A1DA-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316008 R03C01
TCGA-DM-A1DB-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316008 R05C01
TCGA-DM-A1HA-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316008 R01C02
TCGA-DM-A1HB-01	Tumor	NA	TCGA COREAD	6929718086 R01C02
TCGA-DM-A280-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6285625085 R04C02
TCGA-DM-A282-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929671163 R04C01
TCGA-DM-A285-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6285625085 R02C01
TCGA-DM-A288-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6285625085 R01C01
TCGA-DM-A28A-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625085 R05C02
TCGA-DM-A28C-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625085 R05C01
TCGA-DM-A28E-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625085 R01C02
TCGA-DM-A28F-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625085 R04C01
TCGA-DM-A28G-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625085 R06C02
TCGA-DM-A28H-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625085 R06C01
TCGA-DM-A28K-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6285625085 R03C01
TCGA-DM-A28M-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6285625076 R06C02
TCGA-DT-5265-01	Tumor	Rectal_Mucinous_Adenocarcinoma	TCGA COREAD	6929718081 R04C01
TCGA-DY-A0XA-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6264509055 R02C01
TCGA-DY-A1DC-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6264509055 R03C01
TCGA-DY-A1DD-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6264509055 R04C01
TCGA-DY-A1DE-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6264509055 R05C01
TCGA-DY-A1DF-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6264509055 R06C01
TCGA-DY-A1DG-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6264509055 R01C02
TCGA-DY-A1H8-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6264509055 R02C02
TCGA-EF-5830-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718042 R05C02
TCGA-EF-5831-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718042 R06C02
TCGA-EI-6506-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424097 R06C01
TCGA-EI-6507-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424097 R03C01
TCGA-EI-6508-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424040 R04C01
TCGA-EI-6509-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424040 R02C02
TCGA-EI-6510-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424075 R06C01
TCGA-EI-6511-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424075 R02C02
TCGA-EI-6512-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424097 R01C01
TCGA-EI-6513-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424075 R05C01
TCGA-EI-6514-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424075 R02C01
TCGA-EI-6881-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718114 R05C02
TCGA-EI-6882-01	Tumor	Rectal_Mucinous_Adenocarcinoma	TCGA COREAD	6929718114 R03C02
TCGA-EI-6883-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718114 R06C01
TCGA-EI-6884-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718114 R02C02
TCGA-EI-6885-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718114 R04C01
TCGA-EI-6917-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718114 R01C02
TCGA-EI-7002-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718113 R05C02
TCGA-EI-7004-01	Tumor	Rectal_Mucinous_Adenocarcinoma	TCGA COREAD	6929718113 R04C02
TCGA-F4-6459-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825028 R03C01
TCGA-F4-6460-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825035 R05C02
TCGA-F4-6461-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825020 R05C02
TCGA-F4-6463-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6042308159 R03C01
TCGA-F4-6569-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825028 R02C02
TCGA-F4-6570-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825020 R06C01
TCGA-F4-6703-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718054 R02C02
TCGA-F4-6704-01	Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6929718065 R03C02
TCGA-F4-6805-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718079 R01C01
TCGA-F4-6806-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718079 R02C01
TCGA-F4-6807-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718079 R03C01
TCGA-F4-6808-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718053 R06C01
TCGA-F4-6809-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718065 R02C02
TCGA-F4-6854-01	Tumor	Colon_Adenocarcinoma	TCGA COREAD	6264509127 R06C01
TCGA-F5-6464-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424040 R05C02
TCGA-F5-6465-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424097 R05C01
TCGA-F5-6571-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718061 R03C01
TCGA-F5-6702-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718061 R04C01
TCGA-F5-6810-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718058 R05C02
TCGA-F5-6811-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718061 R04C02
TCGA-F5-6812-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718081 R02C02
TCGA-F5-6813-01	Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718081 R06C01

TCGA-F5-6814-01		Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718113 R06C02
TCGA-F5-6861-01		Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718114 R01C01
TCGA-F5-6863-01		Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718114 R03C01
TCGA-F5-6864-01		Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718114 R04C02
TCGA-G4-6293-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308159 R06C01
TCGA-G4-6294-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825035 R04C02
TCGA-G4-6295-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308165 R05C02
TCGA-G4-6297-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316001 R05C01
TCGA-G4-6298-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316015 R02C01
TCGA-G4-6299-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825002 R04C01
TCGA-G4-6302-01		Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6042308158 R05C01
TCGA-G4-6303-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825002 R01C01
TCGA-G4-6306-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825028 R05C01
TCGA-G4-6307-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308158 R04C01
TCGA-G4-6309-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718053 R05C02
TCGA-G4-6310-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316001 R03C02
TCGA-G4-6311-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308159 R04C02
TCGA-G4-6314-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316011 R02C01
TCGA-G4-6315-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308158 R06C01
TCGA-G4-6317-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316015 R04C02
TCGA-G4-6320-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316015 R03C01
TCGA-G4-6321-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042308158 R01C02
TCGA-G4-6322-01		Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	6042308158 R02C02
TCGA-G4-6323-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6042316001 R02C02
TCGA-G4-6586-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825020 R01C01
TCGA-G4-6588-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825002 R06C01
TCGA-G4-6625-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825028 R02C01
TCGA-G4-6626-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825002 R03C01
TCGA-G4-6627-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6057825002 R02C01
TCGA-G4-6628-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	6929718065 R04C02
TCGA-G5-6233-01		Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424097 R02C01
TCGA-G5-6235-01		Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6055424040 R05C01
TCGA-G5-6572-01		Tumor	Rectal_Adenocarcinoma	TCGA COREAD	6929718061 R03C02
TCGA-G5-6641-01		Tumor	Rectal_Mucinous_Adenocarcinoma	TCGA COREAD	6929718061 R02C01
TCGA-NH-A50T-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	9296931074 R03C01
TCGA-NH-A50U-01		Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	9702496157 R05C02
TCGA-NH-A50V-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	9296931073 R02C01
TCGA-NH-A5IV-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	9702496157 R06C02
TCGA-NH-A6GA-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	9702496157 R01C02
TCGA-NH-A6GB-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	9702496157 R04C01
TCGA-NH-A6GC-01		Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	3999492120 R04C01
TCGA-NH-A8F7-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	3999492120 R05C02
TCGA-NH-A8F8-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	3999492120 R01C02
TCGA-QG-A5YV-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	9296931074 R05C01
TCGA-QG-A5YW-01		Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	9296931073 R04C02
TCGA-QG-A5YX-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	9296931073 R03C01
TCGA-QG-A5Z1-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	9296931074 R01C01
TCGA-QG-A5Z2-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	9296931073 R05C02
TCGA-QL-A97D-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	3999492120 R02C01
TCGA-RU-A8FL-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	9702496157 R02C01
TCGA-SS-A7HO-01		Tumor	NA	TCGA COREAD	9702496157 R03C01
TCGA-T9-A92H-01		Tumor	Colon_Adenocarcinoma	TCGA COREAD	9702496157 R04C02
TCGA-WS-AB45-01		Tumor	Colon_Mucinous_Adenocarcinoma	TCGA COREAD	3999492120 R01C01
	3331	Normal_mucosa	Healthy	GSE48684	
	3332	Normal_mucosa	Healthy	GSE48684	
	3333	Normal_mucosa	Healthy	GSE48684	
	3999	Normal_mucosa	Healthy	GSE48684	
	4000	Normal_mucosa	Healthy	GSE48684	
	4001	Normal_mucosa	Healthy	GSE48684	
	4002	Normal_mucosa	Healthy	GSE48684	
	4003	Normal_mucosa	Healthy	GSE48684	
	4004	Normal_mucosa	Healthy	GSE48684	
	4005	Normal_mucosa	Healthy	GSE48684	
	4006	Normal_mucosa	Healthy	GSE48684	
	3325	Normal_mucosa	Healthy	GSE48684	
	3326	Normal_mucosa	Healthy	GSE48684	
	3327	Normal_mucosa	Healthy	GSE48684	
	3328	Normal_mucosa	Healthy	GSE48684	
	3329	Normal_mucosa	Healthy	GSE48684	
	3330	Normal_mucosa	Healthy	GSE48684	
CCR141		Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
CCR169		Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
	5802	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
	9043	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
	9579	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
	11827	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
	11839	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
	11879	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
	3212	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
	9047	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
	11831	Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
CCR221		Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
CCR209		Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
CCR281		Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
CCR289		Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
CCR253		Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
CCR197		Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
CCR193		Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
CCR217		Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
CCR185		Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
CCR181		Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
CCR233		Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
CCR139		Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	
CCR277		Normal_mucosa	Colon_Adenocarcinoma_norm	GSE48684	

Supplementary File 2B

Differentially methylated probes identified with exclusion criteria

Probe_ID	CHR	MAPINFO	arm	gene	distancetoGene	feature	cgi	feat.cgi	conserved_tfbs	Exclusion criteria
cg09248054	1	969257	p	AGRN	NA	Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg27541454	1	975551	p	AGRN	NA	Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg22497741	1	1475644	p	C1orf70	NA	Body	shore	Body - shore	NA	Within telomer region
cg16306898	1	1475675	p	C1orf70	NA	1stExon	shore	1stExon - shore	NA	Within telomer region
cg16601494	1	1475737	p	C1orf70	NA	5'UTR	shore	5'UTR - shore	V$P53_01	Positivity in blood
cg15487867	1	1475742	p	C1orf70	NA	TSS200	shore	TSS200 - shore	V$P53_01	Within telomer region
cg24368383	1	1565856	p	MIB2	NA	Body	island	Body - island	V$MYOGNF1_01	Not overlapping Differentially Methylated Region
cg04021697	1	3567303	p	WDR8	NA	TSS1500	island	TSS1500 - island	NA	Positivity in blood
cg15472784	1	3663531	p	KIAA0495	NA	1stExon	island	1stExon - island	NA	Within telomer region
cg25467973	1	3663705	p	KIAA0495	NA	1stExon	island	1stExon - island	NA	Within telomer region
cg05121790	1	12123554	p	TNFRSF8	NA	5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg21819468	1	13910569	p	PDPN	NA	TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg17456100	1	22140859	p	LDLRAD2	NA	Body	shore	Body - shore	NA	Too far from other differentially methylated probes (>150bp)
cg15467646	1	22141014	p	LDLRAD2	NA	Body	island	Body - island	NA	Too far from other differentially methylated probes (>150bp)
cg24685006	1	36043014	p	TFAP2E	NA	Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg08599259	1	38510933	p	POU3F1	NA	3'UTR	island	3'UTR - island	NA	Not overlapping Differentially Methylated Region
cg23671221	1	44031300	p	PTPRF	NA	Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg04023150	1	44873064	p	RNF220	NA	5'UTR	island	5'UTR - island	NA	Too far from other differentially methylated probes (>150bp)
cg10224098	1	44873229	p	RNF220	NA	5'UTR	island	5'UTR - island	NA	Positivity in blood
cg16732616	1	50886782	p	DMRTA2	NA	Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg19166660	1	57889035	p	DAB1	NA	5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg05375728	1	58715539	p	DAB1	NA	5'UTR	island	5'UTR - island	NA	Selected probes
cg27510182	1	58715553	p	DAB1	NA	5'UTR	island	5'UTR - island	NA	Selected probes
cg02283366	1	63785544	p	FOXD3	-3186	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg25339566	1	67218165	p	TCTEX1D1	NA	5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg14520424	1	70034491	p	PIN1P1	-191367	IGR	island	IGR - island	NA	Too far from other differentially methylated probes (>150bp)
cg08146483	1	75602412	p	LHX8	NA	Body	island	Body - island	NA	Positivity in blood
cg13463054	1	77333159	p	ST6GALNAC5	NA	TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg04077662	1	77333229	p	ST6GALNAC5	NA	1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg25026529	1	91183051	p	BARHL2	NA	TSS1500	shore	TSS1500 - shore	V$USF_C	Not overlapping Differentially Methylated Region
cg24884703	1	91185422	p	BARHL2	7843	IGR	island	IGR - island	V$E2F_02	Not overlapping Differentially Methylated Region
cg22333214	1	98511789	p	MIR137	NA	TSS200	shore	TSS200 - shore	NA	Not overlapping Differentially Methylated Region
cg14991984	1	99470129	p	LPPR5	NA	1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg06543087	1	108508548	p	VAV3	NA	TSS1500	shore	TSS1500 - shore	NA	Not overlapping Differentially Methylated Region
cg20302133	1	111217194	p	KCNA3	NA	1stExon	island	1stExon - island	NA	Within centromer region
cg26013553	1	111217406	p	KCNA3	NA	1stExon	island	1stExon - island	NA	Within centromer region
cg11595545	1	111217497	p	KCNA3	NA	1stExon	island	1stExon - island	NA	Within centromer region
cg01423964	1	111217575	p	KCNA3	NA	1stExon	island	1stExon - island	V$NRSF_01	Within centromer region
cg06750832	1	111217691	p	KCNA3	NA	TSS200	island	TSS200 - island	NA	Within centromer region
cg07808555	1	111217712	p	KCNA3	NA	TSS200	island	TSS200 - island	NA	Within centromer region
cg14175690	1	119527638	p	TBX15	NA	5'UTR	shore	5'UTR - shore	NA	Positivity in blood
cg01439876	1	119543336	p	WARS2	-30503	IGR	island	IGR - island	NA	Positivity in blood
cg01959730	1	119548825	p	WARS2	-25014	IGR	shore	IGR - shore	NA	Positivity in blood
cg02457680	1	154475139	q	TDRD10	NA	5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg23089825	1	170630558	q	PRRX1	-2755	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg16993043	1	200008026	q	NR5A2	NA	Body	shore	Body - shore	NA	Not overlapping Differentially Methylated Region
cg09557387	1	207818395	q	CR1L	NA	TSS200	island	TSS200 - island	NA	Positivity in blood
cg07914084	1	237205999	q	RYR2	NA	Body	island	Body - island	NA	Positivity in blood
cg02328010	1	237206482	q	RYR2	NA	Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg18863333	2	5833195	p	SOX11	NA	1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg04043795	2	5836366	p	SOX11	NA	3'UTR	island	3'UTR - island	NA	Not overlapping Differentially Methylated Region
cg06333058	2	29338077	p	CLIP4	NA	TSS1500	island	TSS1500 - island	NA	Selected probes
cg25737323	2	29338100	p	CLIP4	NA	TSS1500	island	TSS1500 - island	V$SPZ1_01	Selected probes
cg23428985	2	29338113	p	CLIP4	NA	TSS200	island	TSS200 - island	NA	Selected probes
cg23255835	2	29338121	p	CLIP4	NA	TSS200	island	TSS200 - island	NA	Selected probes
cg03135351	2	29338258	p	CLIP4	NA	TSS200	island	TSS200 - island	NA	Selected probes
cg08808128	2	29338432	p	CLIP4	NA	1stExon	island	1stExon - island	NA	Too far from other differentially methylated probes (>150bp)
cg16439198	2	38302674	p	CYP1B1	NA	5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg14411266	2	40679582	p	SLC8A1	NA	5'UTR	shore	5'UTR - shore	NA	Not overlapping Differentially Methylated Region
cg22884656	2	45157296	p	SIX3	-11741	IGR	shore	IGR - shore	NA	Not overlapping Differentially Methylated Region
cg23325963	2	45160093	p	SIX3	-8944	IGR	island	IGR - island	NA	Positivity in blood
cg03714619	2	45160445	p	SIX3	-8592	IGR	shore	IGR - shore	NA	Positivity in blood
cg02155398	2	45160490	p	SIX3	-8547	IGR	shore	IGR - shore	NA	Positivity in blood
cg00097146	2	45171818	p	SIX3	NA	Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg17526573	2	50574708	p	NRXN1	NA	Body	island	Body - island	NA	Positivity in blood
cg27364741	2	63281069	p	OTX1	NA	Body	island	Body - island	NA	Selected probes
cg25622366	2	63281139	p	OTX1	NA	Body	island	Body - island	NA	Selected probes
cg04654530	2	63282702	p	OTX1	NA	Body	island	Body - island	NA	Positivity in blood
cg07974511	2	63283013	p	OTX1	NA	Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg21472506	2	63283967	p	OTX1	NA	3'UTR	island	3'UTR - island	NA	Selected probes
cg23229261	2	63284066	p	OTX1	NA	3'UTR	island	3'UTR - island	NA	Selected probes
cg10122865	2	63284132	p	OTX1	NA	3'UTR	island	3'UTR - island	NA	Selected probes
cg11536474	2	63286049	p	OTX1	8112	IGR	island	IGR - island	NA	Positivity in blood
cg11573679	2	68546467	p	CNRIP1	NA	1stExon	island	1stExon - island	NA	Selected probes
cg07080358	2	68546507	p	CNRIP1	NA	1stExon	island	1stExon - island	NA	Selected probes
cg24171907	2	68546579	p	CNRIP1	NA	1stExon	island	1stExon - island	NA	Selected probes
cg19656282	2	74742786	p	TLX2	NA	Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg21185289	2	74743437	p	TLX2	NA	3'UTR	island	3'UTR - island	NA	Not overlapping Differentially Methylated Region
cg08189989	2	105459164	q	POU3F3	-12805	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg17529832	2	105461096	q	POU3F3	-10873	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg21858380	2	119916486	q	C1QL2	NA	TSS200	island	TSS200 - island	NA	Positivity in blood
cg07212778	2	119916510	q	C1QL2	NA	TSS200	island	TSS200 - island	NA	Too far from other differentially methylated probes (>150bp)
cg15975865	2	127413831	q	GYPC	NA	5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg19484420	2	127414108	q	GYPC	NA	Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg26820055	2	131721099	q	ARHGEF4	NA	Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg26210445	2	162273326	q	TBR1	NA	1stExon	island	1stExon - island	NA	Positivity in blood
cg20935165	2	172972840	q	DLX2	8674	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg06952671	2	182322268	q	ITGA4	NA	5'UTR	island	5'UTR - island	NA	Selected probes
cg21995919	2	182322279	q	ITGA4	NA	5'UTR	island	5'UTR - island	NA	Selected probes
cg25024074	2	182322501	q	ITGA4	NA	1stExon	island	1stExon - island	NA	Too far from other differentially methylated probes (>150bp)
cg11947981	2	182322749	q	ITGA4	NA	Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg16918905	2	220361609	q	GMPPA	-1978	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg00793935	2	234847769	q	TRPM8	NA	Body	island	Body - island	NA	Positivity in blood
cg10429608	2	238864632	q	UBE2F-SCLY	-10955	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg23141355	3	44063593	p	MIR138-1	-92111	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg22702772	3	48699012	p	CELSR3	NA	1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg20072171	3	62356962	p	FEZF2	NA	Body	island	Body - island	V$FAC1_01	Not overlapping Differentially Methylated Region
cg08668199	3	127795571	q	RUVBL1	-4229	IGR	island	IGR - island	NA	Positivity in blood
cg11940285	3	129693385	q	TRH	NA	5'UTR	island	5'UTR - island	NA	Positivity in blood
cg22512438	3	129693489	q	TRH	NA	5'UTR	island	5'UTR - island	NA	Selected probes
cg02700891	3	129693586	q	TRH	NA	5'UTR	island	5'UTR - island	NA	Selected probes
cg17373442	3	142839991	q	CHST2	NA	Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg12892506	3	147113918	q	ZIC4	NA	Body	island	Body - island	NA	Positivity in blood
cg14768785	3	172166517	q	GHSR	NA	TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg07393736	3	172167810	q	GHSR	2477	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg02119363	3	179754603	q	PEX5L	NA	TSS200	island	TSS200 - island	NA	Selected probes
cg13473356	3	179754613	q	PEX5L	NA	TSS200	island	TSS200 - island	NA	Selected probes
cg18780412	3	179755086	q	PEX5L	NA	TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg24000814	3	184301730	q	EPHB3	22143	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg16376000	3	192127330	q	FGF12	NA	TSS1500	island	TSS1500 - island	NA	Positivity in blood
cg17393267	3	192127356	q	FGF12	NA	TSS1500	island	TSS1500 - island	NA	Within telomer region
cg08002883	3	192127457	q	FGF12	NA	TSS1500	island	TSS1500 - island	NA	Within telomer region
cg22834653	3	192232077	q	FGF12	NA	Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg17128947	4	779480	p	CPLX1	NA	3'UTR	island	3'UTR - island	NA	Positivity in blood
cg17397631	4	779880	p	CPLX1	NA	3'UTR	island	3'UTR - island	NA	Positivity in blood
cg27655158	4	1396593	p	CRIPAK	11253	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg14602530	4	4859772	p	MSX1	-1620	IGR	island	IGR - island	V$IK1_01;V$IK3_01	Positivity in blood
cg15092343	4	4860061	p	MSX1	NA	TSS1500	island	TSS1500 - island	NA	Positivity in blood

cg23300732	4	5053496	p	STK32B	NA		TSS200	island	TSS200 - island	NA	Within telomer region
cg08323075	4	5053504	p	STK32B	NA		TSS200	island	TSS200 - island	NA	Within telomer region
cg04575395	4	5892072	p	CRMP1	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg18790597	4	17783331	p	FAM184B	NA		TSS200	island	TSS200 - island	NA	Too far from other differentially methylated probes (>150bp)
cg07696699	4	17783502	p	FAM184B	NA		TSS1500	island	TSS1500 - island	NA	Positivity in blood
cg07907386	4	41749443	p	PHOX2B	NA		Body	island	Body - island	NA	Positivity in blood
cg24657817	4	42153708	p	BEND4	NA		Body	island	Body - island	V$MYOGNF1_01	Not overlapping Differentially Methylated Region
cg23209990	4	55097576	q	PDGFRA	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg05754435	4	55992155	q	KDR	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg13139972	4	107957430	q	DKK2	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg04188273	4	110223830	q	COL25A1	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg21077559	4	122686319	q	TMEM155	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg04638468	4	122686453	q	TMEM155	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg08553437	4	122686456	q	TMEM155	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg07978472	4	122686493	q	TMEM155	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg23901852	4	126238384	q	FAT4	NA		1stExon	island	1stExon - island	V$TAXCREB_01	Not overlapping Differentially Methylated Region
cg10196720	4	134069593	q	PCDH10	NA		TSS1500	island	TSS1500 - island	NA	Positivity in blood
cg17504999	4	134072723	q	PCDH10	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg03112087	4	142053720	q	RNF150	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg15042811	4	144621971	q	FREM3	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg24199834	4	147560126	q	POU4F2	NA		1stExon	island	1stExon - island	NA	Positivity in blood
cg16887264	4	147561775	q	POU4F2	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg00699993	4	158141570	q	GRIA2	NA		TSS200	island	TSS200 - island	NA	Positivity in blood
cg26814276	4	172734266	q	GALNTL6	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg15707093	4	174450353	q	NBLA00301	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg14732324	5	528621	p	MIR4456		-7334	IGR	island	IGR - island	NA	Within telomer region
cg14564616	5	1876337	p	IRX4		-1204	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg06585708	5	3602413	p	IRX1		6245	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg08466792	5	3603227	p	IRX1		7059	IGR	shore	IGR - shore	NA	Not overlapping Differentially Methylated Region
cg25092681	5	16180033	p	MARCH11	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg00339556	5	16180048	p	MARCH11	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg01791874	5	16180055	p	MARCH11	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg17030173	5	16180062	p	MARCH11	NA		TSS200	island	TSS200 - island	NA	Positivity in blood
cg17712694	5	16180068	p	MARCH11	NA		TSS200	island	TSS200 - island	NA	Positivity in blood
cg16150752	5	16180072	p	MARCH11	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg21901718	5	16180076	p	MARCH11	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg23065934	5	16180266	p	MARCH11	NA		TSS1500	island	TSS1500 - island	NA	Positivity in blood
cg10932018	5	54516487	q	MCIDAS		1062	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg18456523	5	54516805	q	MCIDAS		1380	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg14608384	5	54516879	q	MCIDAS		1454	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg18250028	5	71015523	q	CARTPT	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg17448335	5	76249776	q	CRHBP	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg04502985	5	77268452	q	AP3B1		-29698	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg23180938	5	115152485	q	CDO1	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg08516516	5	115152492	q	CDO1	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg11036833	5	115152494	q	CDO1	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg22488797	5	134363324	q	PITX1		-100	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg18443359	5	134374693	q	PITX1		11269	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg01283246	5	135266135	q	FBXL21	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg24847829	5	136834464	q	SPOCK1	NA		5'UTR	island	5'UTR - island	NA	Selected probes
cg14650610	5	136834492	q	SPOCK1	NA		5'UTR	island	5'UTR - island	NA	Selected probes
cg23445461	5	140864733	q	PCDHGA4	NA		Body	island	Body - island	NA	Positivity in blood
cg20755170	5	145720024	q	POU4F3	NA		3'UTR	island	3'UTR - island	NA	Not overlapping Differentially Methylated Region
cg07136998	5	168728081	q	SLIT3	NA		5'UTR	island	5'UTR - island	NA	Positivity in blood
cg18705773	5	170743564	q	TLX3		7276	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg05560435	5	172671526	q	NKX2-5		12419	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg17228900	6	391764	p	IRF4	NA		5'UTR	island	5'UTR - island	NA	Within telomer region
cg06392169	6	391936	p	IRF4	NA		5'UTR	island	5'UTR - island	NA	Within telomer region
cg21277995	6	393239	p	IRF4	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg00110654	6	10385489	p	TFAP2A-AS1		-11427	IGR	island	IGR - island	NA	Positivity in blood
cg24452128	6	10390919	p	TFAP2A-AS1		-5997	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg17754510	6	10391412	p	TFAP2A-AS1		-5504	IGR	shore	IGR - shore	NA	Not overlapping Differentially Methylated Region
cg05452406	6	10881891	p	GCM2	NA		Body	island	Body - island	NA	Positivity in blood
cg10903903	6	27647843	p	LINC01012		-13971	IGR	island	IGR - island	NA	Positivity in blood
cg15490715	6	29521568	p	UBD		-1821	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg22617773	6	29521751	p	UBD		-1638	IGR	island	IGR - island	NA	Selected probes
cg14278853	6	29521756	p	UBD		-1633	IGR	island	IGR - island	NA	Selected probes
cg17394649	6	29760164	p	HCG4	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg27011480	6	30228083	p	HLA-L	NA		Body	island	Body - island	NA	Positivity in blood
cg27200446	6	41606439	p	MDFI	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg01883425	6	41606770	p	MDFI	NA		Body	shore	Body - shore	NA	Not overlapping Differentially Methylated Region
cg18884037	6	62996214	q	KHDRBS2	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg05447008	6	73331114	q	KCNQ5	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg00852573	6	73331405	q	KCNQ5	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg16334314	6	84418789	q	SNAP91	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg14367020	6	99292286	q	POU3F2		9706	IGR	shore	IGR - shore	NA	Positivity in blood
cg17386213	6	108488335	q	NR2E1	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg05085230	6	133562461	q	EYA4	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg08712932	6	133562463	q	EYA4	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg11664500	6	133562479	q	EYA4	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg14287112	6	133562485	q	EYA4	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg22871668	6	133562492	q	EYA4	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg00356183	7	751833	p	PRKAR1B	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg08558397	7	752149	p	PRKAR1B	NA		5'UTR	island	5'UTR - island	NA	Within telomer region
cg16305865	7	752180	p	PRKAR1B	NA		5'UTR	shore	5'UTR - shore	NA	Within telomer region
cg20381963	7	752238	p	PRKAR1B	NA		5'UTR	shore	5'UTR - shore	NA	Positivity in blood
cg18601167	7	752286	p	PRKAR1B	NA		5'UTR	shore	5'UTR - shore	NA	Within telomer region
cg13895235	7	752292	p	PRKAR1B	NA		5'UTR	shore	5'UTR - shore	NA	Within telomer region
cg23244488	7	19146032	p	TWIST1		-9059	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg02400740	7	19157938	p	TWIST1	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg24885417	7	24323764	p	NPY	NA		TSS200	island	TSS200 - island	NA	Positivity in blood
cg16964348	7	24323799	p	NPY	NA		TSS200	island	TSS200 - island	NA	Positivity in blood
cg25884711	7	24323840	p	NPY	NA		5'UTR	island	5'UTR - island	NA	Positivity in blood
cg21097881	7	24323939	p	NPY	NA		5'UTR	island	5'UTR - island	NA	Positivity in blood
cg24245418	7	24324976	p	NPY	NA		Body	island	Body - island	NA	Positivity in blood
cg21773872	7	30722320	p	CRHR2	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg05809668	7	35301188	p	TBX20		30076	IGR	island	IGR - island	NA	Positivity in blood
cg17093995	7	49815502	p	VWC2	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg19868631	7	54609776	p	VSTM2A	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg02300154	7	70597058	q	WBSCR17	NA		TSS1500	island	TSS1500 - island	NA	Too far from other differentially methylated probes (>150bp)
cg03044249	7	70597065	q	WBSCR17	NA		TSS1500	island	TSS1500 - island	NA	Positivity in blood
cg05223720	7	71801793	q	CALN1	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg12973591	7	93519473	q	TFPI2	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg20230721	7	93519855	q	TFPI2	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg16934178	7	93520074	q	TFPI2	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg01307939	7	98467571	q	TMEM130	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg07697895	7	116963259	q	WNT2	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg04153784	7	127672235	q	SND1	NA		Body	island	Body - island	NA	Too far from other differentially methylated probes (>150bp)
cg12628196	7	127672458	q	SND1	NA		Body	island	Body - island	NA	Positivity in blood
cg09087503	7	127672473	q	SND1	NA		Body	island	Body - island	NA	Selected probes
cg09296001	7	127672564	q	SND1	NA		Body	island	Body - island	NA	Selected probes
cg12345672	7	127672658	q	SND1	NA		Body	island	Body - island	NA	Selected probes
cg03514404	7	143579665	q	FAM115A	NA		5'UTR	shelf	5'UTR - shelf	NA	Selected probes
cg01030534	7	143579698	q	FAM115A	NA		5'UTR	shelf	5'UTR - shelf	NA	Selected probes
cg03225210	7	143579951	q	FAM115A	NA		5'UTR	shelf	5'UTR - shelf	NA	Too far from other differentially methylated probes (>150bp)
cg02864844	7	149917263	q	ACTR3C		-27038	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg21532325	7	151107400	q	WDR86	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg19814400	7	158936632	q	VIPR2	NA		Body	island	Body - island	NA	Within telomer region
cg21038156	7	158936739	q	VIPR2	NA		Body	island	Body - island	NA	Within telomer region
cg18349835	7	158937107	q	VIPR2	NA		Body	island	Body - island	NA	Within telomer region
cg03976877	7	158937610	q	VIPR2	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg01200640	8	687384	p	ERICH1		73184	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region

cg26777883	8	688417	p	ERICH1		74217	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg04218812	8	9763263	p	MIR124-1		2365	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg18577280	8	16884549	p	EFHA2	NA		TSS200	island	TSS200 - island	NA	Too far from other differentially methylated probes (>150bp)
cg19677607	8	24772270	p	NEFM	NA		TSS200	island	TSS200 - island	V$LMO2COM_01	Not overlapping Differentially Methylated Region
cg04118306	8	24772350	p	NEFM	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg03169018	8	24772435	p	NEFM	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg04555373	8	31497042	p	NRG1	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg24946597	8	31497464	p	NRG1	NA		5'UTR	island	5'UTR - island	NA	Positivity in blood
cg21517947	8	41167107	p	SFRP1	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg05166490	8	41754172	p	ANK1	NA		1stExon	island	1stExon - island	NA	Within centromer region
cg17331296	8	41754181	p	ANK1	NA		1stExon	island	1stExon - island	NA	Within centromer region
cg15531403	8	53852184	q	NPBWR1	NA		TSS1500	island	TSS1500 - island	NA	Positivity in blood
cg07770968	8	53852422	q	NPBWR1	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg16491617	8	54164391	q	OPRK1	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg11071231	8	57069907	q	PLAG1		-3561	IGR	island	IGR - island	NA	Selected probes
cg16504626	8	57070013	q	PLAG1		-3455	IGR	island	IGR - island	NA	Selected probes
cg04612444	8	57358713	q	PENK	NA		5'UTR	island	5'UTR - island	NA	Positivity in blood
cg25260137	8	65282185	q	LINC00966		-3590	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg25900085	8	65291513	q	MIR124-2	NA		TSS200	shore	TSS200 - shore	NA	Positivity in blood
cg18065361	8	67344588	q	ADHFE1	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg20295442	8	67344665	q	ADHFE1	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg20912169	8	67344720	q	ADHFE1	NA		5'UTR	island	5'UTR - island	NA	Selected probes
cg14353137	8	67873799	q	TCF24		15063	IGR	island	IGR - island	NA	Too far from other differentially methylated probes (>150bp)
cg20980783	8	67874178	q	TCF24		15442	IGR	island	IGR - island	NA	Selected probes
cg26618965	8	67874206	q	TCF24		15470	IGR	island	IGR - island	NA	Selected probes
cg22001496	8	69243486	q	MIR548H4		529	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg21479226	8	69244510	q	MIR548H4		1553	IGR	shore	IGR - shore	NA	Not overlapping Differentially Methylated Region
cg25832771	8	72756058	q	MSC	NA		1stExon	island	1stExon - island	NA	Selected probes
cg09734791	8	72756155	q	MSC	NA		1stExon	island	1stExon - island	V$E47_01	Selected probes
cg05690644	8	97158015	q	GDF6	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg13211683	8	97171827	q	GDF6	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg00421139	8	97172961	q	GDF6	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg18233405	8	98290148	q	TSPYL5	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg16462462	8	117950825	q	C8orf85	NA		Body	shore	Body - shore	NA	Positivity in blood
cg13912117	8	132054555	q	ADCY8		262008	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg17698295	8	145106299	q	OPLAH	NA		Body	island	Body - island	NA	Within telomer region
cg17301223	8	145106438	q	OPLAH	NA		Body	island	Body - island	NA	Within telomer region
cg22882523	8	145107012	q	OPLAH	NA		Body	island	Body - island	NA	Positivity in blood
cg14058647	9	88137909	q	AGTPBP1		-23545	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg24393316	9	100616469	q	FOXE1	NA		1stExon	island	1stExon - island	V$TAXCREB_01	Positivity in blood
cg24039697	10	8094534	p	FLJ45983	NA		Body	island	Body - island	NA	Positivity in blood
cg18794404	10	22542024	p	LOC100130992		1023	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg05099508	10	22634432	p	SPAG6	NA		1stExon	island	1stExon - island	NA	Selected probes
cg24031355	10	22634439	p	SPAG6	NA		1stExon	island	1stExon - island	NA	Selected probes
cg23068913	10	23463377	p	PTF1A		-18083	IGR	island	IGR - island	NA	Positivity in blood
cg24487076	10	23983496	p	KIAA1217	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg13882278	10	23983498	p	KIAA1217	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg08539841	10	23983538	p	KIAA1217	NA		TSS200	island	TSS200 - island	V$AHRARNT_01	Not overlapping Differentially Methylated Region
cg07825347	10	43600497	q	RET	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg06365057	10	50323706	q	C10orf72	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg20744625	10	64578469	q	EGR2	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg06419761	10	72043661	q	LRRC20		-15068	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg11036831	10	82116382	q	DYDC2	NA		TSS200	island	TSS200 - island	NA	Too far from other differentially methylated probes (>150bp)
cg03701427	10	82117089	q	DYDC1	NA		TSS1500	island	TSS1500 - island	NA	Positivity in blood
cg05316043	10	83634974	q	NRG3	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg17538572	10	94834763	q	CYP26A1	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg17863743	10	100993587	q	HPSE2	NA		Body	shore	Body - shore	NA	Not overlapping Differentially Methylated Region
cg12118269	10	102893980	q	TLX1	NA		Body	island	Body - island	NA	Selected probes
cg24812837	10	102894120	q	TLX1	NA		Body	island	Body - island	NA	Selected probes
cg14861089	10	102895043	q	TLX1	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg05482942	10	102899285	q	TLX1		8224	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg14038391	10	102900130	q	TLX1		9069	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg17101450	10	102900365	q	TLX1		9304	IGR	shore	IGR - shore	NA	Not overlapping Differentially Methylated Region
cg25209842	10	103536342	q	FGF8	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg23095743	10	104000831	q	PITX3	NA		5'UTR	island	5'UTR - island	NA	Positivity in blood
cg21384402	10	105036701	q	INA	NA		TSS1500	island	TSS1500 - island	NA	Selected probes
cg24680586	10	105036727	q	INA	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg18932798	10	105037503	q	INA	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg02320740	10	106400259	q	SORCS3	NA		TSS1500	island	TSS1500 - island	NA	Too far from other differentially methylated probes (>150bp)
cg14752336	10	106400454	q	SORCS3	NA		TSS1500	island	TSS1500 - island	NA	Too far from other differentially methylated probes (>150bp)
cg03958798	10	106400686	q	SORCS3	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg13320291	10	118030970	q	GFRA1	NA		Body	island	Body - island	V$OLF1_01;V$ROAZ_01	Not overlapping Differentially Methylated Region
cg05667348	10	118892581	q	VAX1	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg24390913	10	118899788	q	VAX1		6987	IGR	island	IGR - island	NA	Positivity in blood
cg19912142	10	119494671	q	EMX2OS		192715	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg14072515	10	125732604	q	CHST15		-34578	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg08701047	10	130085199	q	MKI67		190274	IGR	open sea	IGR - open sea	NA	Not overlapping Differentially Methylated Region
cg27513573	10	131768098	q	CTAGE7P		-94064	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg03109827	10	133110349	q	TCERG1L	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg02886408	10	133796164	q	BNIP3	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg12816961	10	134598927	q	NKX6-2	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg25774643	11	627175	p	SCT	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg12928379	11	637175	p	DRD4	NA		TSS200	island	TSS200 - island	NA	Within telomer region
cg09607276	11	637491	p	DRD4	NA		1stExon	island	1stExon - island	NA	Within telomer region
cg25098208	11	8190659	p	RIC3	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg02027945	11	20618230	p	SLC6A5		-2716	IGR	island	IGR - island	NA	Positivity in blood
cg01642521	11	20618250	p	SLC6A5		-2696	IGR	island	IGR - island	NA	Positivity in blood
cg14749465	11	20690720	p	NELL1	NA		TSS1500	island	TSS1500 - island	NA	Selected probes
cg02510267	11	20690807	p	NELL1	NA		TSS1500	island	TSS1500 - island	NA	Selected probes
cg23861668	11	20691126	p	NELL1	NA		5'UTR	island	5'UTR - island	NA	Selected probes
cg14689623	11	20691161	p	NELL1	NA		5'UTR	island	5'UTR - island	NA	Selected probes
cg01563031	11	20691429	p	NELL1	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg09537620	11	31826574	p	PAX6	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg18372607	11	31827084	p	PAX6	NA		Body	shore	Body - shore	NA	Not overlapping Differentially Methylated Region
cg26848718	11	32454975	p	WT1	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg15556502	11	43602845	p	MIR129-2	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg14416371	11	43602847	p	MIR129-2	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg14944647	11	43602857	p	MIR129-2	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg01939477	11	43602879	p	MIR129-2	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg05376374	11	43602920	p	MIR129-2	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg09802835	11	71952131	q	PHOX2A	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg04543008	11	71955332	q	PHOX2A	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg03225817	11	105481317	q	GRIA4	NA		5'UTR	island	5'UTR - island	NA	Selected probes
cg04747226	11	105481319	q	GRIA4	NA		5'UTR	island	5'UTR - island	NA	Selected probes
cg07972135	11	105481322	q	GRIA4	NA		5'UTR	island	5'UTR - island	NA	Selected probes
cg22879515	11	111383515	q	MIR34B	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg09657963	11	124790875	q	HEPACAM	NA		3'UTR	island	3'UTR - island	NA	Positivity in blood
cg03419885	11	125036385	q	PKNOX2	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg23727983	11	125774082	q	DDX25	NA		TSS200	shore	TSS200 - shore	NA	Selected probes
cg01736784	11	125774092	q	DDX25	NA		TSS200	shore	TSS200 - shore	NA	Selected probes
cg11017065	11	128564874	q	FLI1	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg07072722	11	131781246	q	NTM	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg06947913	12	50297793	q	FAIM2	NA		TSS200	island	TSS200 - island	NA	Too far from other differentially methylated probes (>150bp)
cg00817367	12	52401214	q	GRASP	NA		Body	island	Body - island	NA	Too far from other differentially methylated probes (>150bp)
cg09597070	12	54088972	q	CALCOCO1		-15930	IGR	shore	IGR - shore	NA	Not overlapping Differentially Methylated Region
cg08190858	12	54321346	q	HOXC13-AS		-7766	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg27277463	12	62585031	q	FAM19A2	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg26272220	12	81471884	q	ACSS3	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg22538054	12	95941988	q	USP44	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg03308628	12	95942287	q	USP44	NA		5'UTR	island	5'UTR - island	NA	Positivity in blood
cg22802813	12	95942761	q	USP44	NA		TSS200	island	TSS200 - island	NA	Positivity in blood
cg01857475	12	104697193	q	TXNRD1	NA		5'UTR	shore	5'UTR - shore	NA	Positivity in blood

cg03817911	12	104697389	q	TXNRD1	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg10790429	12	106974623	q	LOC100287944		-2062	IGR	island	IGR - island	NA	Positivity in blood
cg11213520	12	113901529	q	LHX5	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg04569082	12	127940323	q	FLJ37505		-425839	IGR	shore	IGR - shore	NA	Not overlapping Differentially Methylated Region
cg09170112	12	132102188	q	SFSWAP		-93444	IGR	open sea	IGR - open sea	NA	Positivity in blood
cg04865180	13	23734385	q	SGCG		-20675	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg19937061	13	25320133	q	RNF17		-18168	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg25366582	13	25621027	q	PABPC3		-49249	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg20194314	13	28503060	q	PDX1		8892	IGR	island	IGR - island	NA	Positivity in blood
cg17200768	13	28503373	q	PDX1		9205	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg02478448	13	37006063	q	CCNA1	NA		1stExon	island	1stExon - island	NA	Positivity in blood
cg18348647	13	37006107	q	CCNA1	NA		1stExon	island	1stExon - island	NA	Too far from other differentially methylated probes (>150bp)
cg08866608	13	58203798	q	PCDH17		-1991	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg20634967	13	58204224	q	PCDH17		-1565	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg23766591	13	78493205	q	EDNRB	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg24236409	13	78493282	q	EDNRB	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg26132774	13	79170146	q	RNF219-AS1		-3084	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg00295794	13	100641409	q	ZIC2		7383	IGR	island	IGR - island	NA	Positivity in blood
cg18115507	13	102069169	q	NALCN	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg11437784	13	112710823	q	SOX1		-11090	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg13692446	13	112759719	q	SOX1		37806	IGR	island	IGR - island	NA	Within telomer region
cg25570913	13	112759893	q	SOX1		37980	IGR	island	IGR - island	NA	Within telomer region
cg15384598	14	24045549	q	JPH4	NA		Body	island	Body - island	V$ER_Q6	Not overlapping Differentially Methylated Region
cg08217024	14	48145108	q	MDGA2	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg19871940	14	57264287	q	OTX2		-3138	IGR	shore	IGR - shore	NA	Not overlapping Differentially Methylated Region
cg21026830	14	60973517	q	SIX6		-2421	IGR	shore	IGR - shore	NA	Not overlapping Differentially Methylated Region
cg06785999	14	60975964	q	SIX6	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg19456540	14	60976285	q	SIX6	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg04281464	14	70014873	q	CCDC177		-21658	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg23241781	14	70653964	q	SLC8A3	NA		5'UTR	shore	5'UTR - shore	NA	Not overlapping Differentially Methylated Region
cg22916722	14	76605056	q	GPATCH2L		-13203	IGR	island	IGR - island	NA	Too far from other differentially methylated probes (>150bp)
cg17410236	14	85996495	q	FLRT2	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg02874376	14	101193397	q	DLK1	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg03419058	15	26108391	q	ATP10A	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg10652393	15	27112430	q	GABRA5	NA		1stExon	island	1stExon - island	V$TAXCREB_01	Not overlapping Differentially Methylated Region
cg04803843	15	28351906	q	HERC2		-4277	IGR	island	IGR - island	NA	Too far from other differentially methylated probes (>150bp)
cg03061682	15	28352098	q	HERC2		-4085	IGR	island	IGR - island	NA	Too far from other differentially methylated probes (>150bp)
cg00330492	15	28352558	q	HERC2		-3625	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg17741501	15	29077493	q	MIR5009		-12614	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg13800209	15	37390284	q	MEIS2	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg02018277	15	65116255	q	PIF1	NA		Body	island	Body - island	NA	Positivity in blood
cg09193347	15	79381867	q	RASGRF1	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg20973720	15	79383167	q	RASGRF1	NA		5'UTR	island	5'UTR - island	V$TAXCREB_02	Not overlapping Differentially Methylated Region
cg11167100	15	83776269	q	TM6SF1	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg08452658	15	83776271	q	TM6SF1	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg26460092	15	83776420	q	TM6SF1	NA		5'UTR	island	5'UTR - island	NA	Selected probes
cg03063639	15	83776422	q	TM6SF1	NA		5'UTR	island	5'UTR - island	NA	Positivity in blood
cg02318926	15	83952345	q	BNC1	NA		Body	island	Body - island	NA	Selected probes
cg23989963	15	83952420	q	BNC1	NA		Body	island	Body - island	NA	Selected probes
cg17124224	15	83953880	q	BNC1	NA		TSS1500	island	TSS1500 - island	NA	Too far from other differentially methylated probes (>150bp)
cg06523224	15	83953883	q	BNC1	NA		TSS1500	island	TSS1500 - island	NA	Positivity in blood
cg19288904	15	98836248	q	FAM169B		-144143	IGR	open sea	IGR - open sea	NA	Positivity in blood
cg05915293	16	2041512	p	SYNGR3	NA		Body	shore	Body - shore	NA	Not overlapping Differentially Methylated Region
cg07642043	16	10276674	p	GRIN2A	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg00133595	16	31228059	p	TRIM72	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg02809746	16	49312033	q	CBLN1		204	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg04698114	16	51184379	q	SALL1	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg08806408	16	51185001	q	SALL1	NA		TSS1500	island	TSS1500 - island	NA	Selected probes
cg00124695	16	51185039	q	SALL1	NA		TSS1500	island	TSS1500 - island	NA	Selected probes
cg08439930	16	51185060	q	SALL1	NA		TSS1500	island	TSS1500 - island	NA	Positivity in blood
cg06653699	16	51185082	q	SALL1	NA		TSS1500	island	TSS1500 - island	NA	Selected probes
cg07502439	16	51185461	q	SALL1	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg01064265	16	55363058	q	IRX6	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg09849405	16	66612955	q	CMTM1	NA		3'UTR	island	3'UTR - island	NA	Not overlapping Differentially Methylated Region
cg08032924	16	66613096	q	CMTM2	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg16626067	16	66613266	q	CMTM2	NA		TSS200	island	TSS200 - island	NA	Positivity in blood
cg06666025	16	66613278	q	CMTM2	NA		TSS200	island	TSS200 - island	NA	Positivity in blood
cg07816687	16	67197186	q	HSF4	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg00748373	16	68676741	q	CDH3	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg16801887	16	86541480	q	FOXF1		-2653	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg16202470	17	8907213	p	NTN1		-17646	IGR	island	IGR - island	V$AP2_Q6	Not overlapping Differentially Methylated Region
cg13291283	17	10101195	p	GAS7	NA		Body	island	Body - island	NA	Too far from other differentially methylated probes (>150bp)
cg25116216	17	10101581	p	GAS7	NA		1stExon	island	1stExon - island	NA	Too far from other differentially methylated probes (>150bp)
cg08358166	17	18538271	p	TBC1D28		-571	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg18686527	17	27044685	q	RAB34	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg21101720	17	27940509	q	ANKRD13B	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg14603098	17	32484259	q	ACCN1	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg15790037	17	37321490	q	ARL5C	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg13001868	17	43339223	q	C17orf46	NA		Body	island	Body - island	NA	Selected probes
cg04992638	17	43339328	q	C17orf46	NA		Body	island	Body - island	NA	Selected probes
cg03048083	17	43339497	q	LOC100133991	NA		Body	island	Body - island	NA	Selected probes
cg01627847	17	43339512	q	LOC100133991	NA		Body	island	Body - island	NA	Selected probes
cg08124910	17	43339515	q	LOC100133991	NA		Body	island	Body - island	NA	Selected probes
cg24542751	17	43339589	q	LOC100133991	NA		Body	island	Body - island	NA	Selected probes
cg02081266	17	59529618	q	TBX4		-4189	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg20275528	17	75369484	q	SEPT9	NA		5'UTR	island	5'UTR - island	NA	Too far from other differentially methylated probes (>150bp)
cg12783819	17	75369657	q	SEPT9	NA		5'UTR	island	5'UTR - island	NA	Too far from other differentially methylated probes (>150bp)
cg12865552	17	77721631	q	ENPP7		16749	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg11771234	18	908396	p	ADCYAP1	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg22455914	18	7116977	p	LAMA1	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg03117976	18	11149435	p	FAM38B	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg25958283	18	11752089	p	GNAL	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg21114773	18	12254452	p	CIDEA	NA		Body	island	Body - island	NA	Positivity in blood
cg12395205	18	12254469	p	CIDEA	NA		Body	island	Body - island	NA	Within centromer region
cg16727201	18	12254556	p	CIDEA	NA		Body	island	Body - island	NA	Positivity in blood
cg05700339	18	12254566	p	CIDEA	NA		Body	island	Body - island	NA	Within centromer region
cg27641522	18	53447560	q	MIR4529		301108	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg07519816	18	53447596	q	MIR4529		301144	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg27189087	18	56941246	q	RAX	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg12799689	18	67067893	q	DOK6	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg18596362	18	70210955	q	CBLN2	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg18448581	18	70534767	q	NETO1	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg05884032	18	76740088	q	SALL3	NA		TSS200	island	TSS200 - island	V$MYOGNF1_01	Positivity in blood
cg14007067	18	76740258	q	SALL3	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg11616651	19	2251837	p	AMH	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg22963915	19	3785855	p	MATK	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg25936054	19	15090242	p	SLC1A6		29251	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg04704053	19	15090275	p	SLC1A6		29284	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg18652900	19	15580445	p	PGLYRP2	NA		Body	island	Body - island	NA	Positivity in blood
cg16206460	19	15580700	p	PGLYRP2	NA		Body	island	Body - island	NA	Positivity in blood
cg08607018	19	31842873	q	TSHZ3		77022	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg25999442	19	34113398	q	CHST8	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg04332534	19	37096487	q	ZNF382	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg11957331	19	42828156	q	TMEM145	NA		Body	island	Body - island	V$TAXCREB_02	Not overlapping Differentially Methylated Region
cg09489306	19	44203913	q	IRGC		-16301	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg15779837	19	48918116	q	GRIN2D	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg22049569	19	54466538	q	CACNG8	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg15708153	19	56879554	q	ZNF542	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg26612735	19	56988806	q	ZNF667	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg08063125	19	56989543	q	ZNF667	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg18845189	19	57683712	q	ZNF264		-19156	IGR	island	IGR - island	NA	Not overlapping Differentially Methylated Region
cg02446106	19	57751691	q	ZNF805	NA		TSS1500	shore	TSS1500 - shore	NA	Not overlapping Differentially Methylated Region

cg18579862	19	58095595	q	ZIK1	NA		TSS200	island	TSS200 - island	NA	Within telomer region
cg13668618	19	58446745	q	ZNF418	NA		TSS200	island	TSS200 - island	NA	Within telomer region
cg12961842	19	58446758	q	ZNF418	NA		TSS200	island	TSS200 - island	NA	Within telomer region
cg12028548	20	590799	p	TCF15	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg07113642	20	2781262	p	CPXM1	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg14262681	20	21084420	p	KIZ		-22204	IGR	shore	IGR - shore	NA	Not overlapping Differentially Methylated Region
cg17368760	20	23029287	p	THBD	NA		1stExon	island	1stExon - island	NA	Selected probes
cg16339238	20	23029298	p	THBD	NA		1stExon	island	1stExon - island	NA	Selected probes
cg22388634	20	25058429	p	VSX1	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg14763548	20	25062447	p	VSX1	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg10615414	20	37353096	q	SLC32A1	NA		TSS200	island	TSS200 - island	NA	Selected probes
cg08313939	20	37353117	q	SLC32A1	NA		5'UTR	island	5'UTR - island	NA	Selected probes
cg24454144	20	37353126	q	SLC32A1	NA		5'UTR	island	5'UTR - island	NA	Selected probes
cg11172693	20	37434229	q	PPP1R16B	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg24033330	20	39317034	q	MAFB	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg03403065	20	41818358	q	PTPRT	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region
cg10439765	20	44657838	q	SLC12A5	NA		1stExon	island	1stExon - island	NA	Positivity in blood
cg14060496	20	61638518	q	BHLHE23	NA		TSS200	island	TSS200 - island	NA	Within telomer region
cg26492446	20	61638574	q	BHLHE23	NA		TSS200	island	TSS200 - island	NA	Within telomer region
cg27501878	20	61638588	q	BHLHE23	NA		TSS1500	island	TSS1500 - island	NA	Within telomer region
cg15699267	20	61809557	q	MIR124-3	NA		TSS1500	island	TSS1500 - island	NA	Not overlapping Differentially Methylated Region
cg27357571	21	34398226	q	OLIG2	NA		TSS200	island	TSS200 - island	NA	Not overlapping Differentially Methylated Region
cg00495860	21	38065524	q	SIM2		-6467	IGR	island	IGR - island	NA	Positivity in blood
cg21697851	21	38076869	q	SIM2	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg10682155	21	38077473	q	SIM2	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg24080247	21	38082613	q	SIM2	NA		Body	shore	Body - shore	NA	Positivity in blood
cg25446076	21	38083149	q	SIM2	NA		Body	shore	Body - shore	NA	Not overlapping Differentially Methylated Region
cg05206884	22	33454324	q	SYN3	NA		5'UTR	island	5'UTR - island	NA	Not overlapping Differentially Methylated Region
cg04198308	22	48971959	q	FAM19A5	NA		Body	island	Body - island	NA	Not overlapping Differentially Methylated Region
cg03957481	22	50986962	q	KLHDC7B	NA		1stExon	island	1stExon - island	NA	Not overlapping Differentially Methylated Region

Supplementary File 2C

Name	5'-->3' Sequence (for Bisulfite converted DNA)	Mg (mM)	Tm (°C)	length (bp)	Taq (unit)	Genomic_location_hg19	Encompassing probes from Illumina Infinium 450k.
Tag1	TCCCGCGAAATTAATACGAC						
Tag2	GCTGGAGCTCTGCAGCTA						
GRIA4-FW	TCCCGCGAAATTAATACGACGGGTTGGTGTAGGTTTGTT	1.5	62	106		chr11:105481255-105481360	cg15603568;cg23559689; cg00343633;cg03225817; cg04747226;cg07972135
GRIA4-RV	GCTGGAGCTCTGCAGCTACTCCCCCCTTACTTTCTCACATACACACAA						
GRIA4-met-Probe	/5Alex647N/AACGCCGCGACCGCCACAC						
GRIA4-unm-Probe	/5Alex488N/CACCACAACCACCACACACA						
MSC-FW	TCCCGCGAAATTAATACGACAGGGTTTAGTAGTAGAGTGTAAGT	1.5	58	122		chr8:72756000-72756121	cg25832771
MSC-RV	GCTGGAGCTCTGCAGCTAAAACACCCAAAACAAACTAATCT						
MSC-met-Probe	/5Alex647N/CGCATCCGAACACGCTCAC						
MSC-unm-Probe	/5Alex488N/ACACATCCAAACACACTCAC						
EYA4-FW	TCCCGCGAAATTAATACGACGTGGATAGGATGGAAGTTT	2	54	96		chr6:133562421-133562516	cg05085230; cg08712932; cg06132028; cg11942956; cg20787173; cg11664500; cg14287112; cg22871668;
EYA4-RV	GCTGGAGCTCTGCAGCTACCCCCCCCCACCTCCCTAC						
EYA4-met-Probe	/5Alex647N/GACCGTTCCCGACTTCCGC						
EYA4-Unmet-Probe	/5Alex488N/CACTCCAACCATTCCCA						
MAP3K14-AS1-FW	TCCCGCGAAATTAATACGACGGATTGGTGGGAGTTGGAAATATTAGA	2.5	50	99		chr17:43339469-43339567	cg17222164; cg03048083; cg01627847; cg08124910
MAP3K14-AS1-RV	GCTGGAGCTCTGCAGCTAACCTAAATACCACTCCCTACCTATAAAAT						
MAP3K14-AS1-met-Probe	/5Alex647N/CGACGACATCACAAACACCGACG						
MAP3K14-AS1-unm-Probe	/5Alex488N/CAACAACATCACAAACACCAACA						
ITGA4-FW	TCCCGCGAAATTAATACGACGGGGAAGAAAGTTTTAAGAGATGAG	2.5	50	76		chr2:182,322,231-182,322,306	cg06952671; cg21995919
ITGA4-RV	GCTGGAGCTCTGCAGCTATCCTCTTCCCTCTCTCCT						
ITGA4-met-Probe	/5Alex647N/ACCCGCTAACGCCGAACACGCTA						
ITGA4-unm-Probe	/5Alex488N/ACCCACTAACACCAAACACACTA						

Name	Catalog #	Tm(°C)
BRAF V600E	dHsaCP2000027	55
KRAS G13D	dHsaMDV2510598	55
KRAS G12D	dHsaMDV2510596	55
KRAS G12A	dHsaMDV2510586	55
KRAS G12R	dHsaMDV2510590	55
KRAS G12V	dHsaMDV2510592	55
KRAS G12C	dHsaMDV2510584	55
KRAS Q61H	dHsaMDV2010131	55
MET CNV	dHsaCP2500321	60

Supplementary File 2D

Clinical data summary for the two cohorts of cfDNA donors involved in the study

Aging Cohort		N	(%)
Sex		25	(50)
		25	(50)
Age (years)		61	
		[40-65]	

mCRC cohort		N	(%)
Sex	Male	117	(64.3)
	Female	65	(35.7)
Age (years)	median	64	
	Range	[33-85]	
CEA (ng/ml)	median	66.1	
	Range	[0.8-20543]	
	<=5	27	(14.9)
	>5	154	(85.1)
	NA	1	(0.6)
# previous treatment lines	0	38	(20.9)
	1	19	(10.4)
	2	43	(23.6)
	3	37	(20.3)
	4+	45	(24.7)
RECIST (mm) (quartiles)	[9-49.25[	44	(24.3)
	[49.25-81.55[	43	(23.8)
	[81.55-117[	42	(23.2)
	[117-250]	45	(24.9)
	NA	7	(3.9)
Primary tumor resected	Yes	150	(82.9)
	No	31	(17.1)
Metastatic lesions	1	49	(26.9)
	2+	128	(70.3)
	NA	5	(2.7)
Bulky Disease	No	122	(67)
	Yes	47	(25.8)
	NA	13	(7.1)
RAS	wild type	107	(58.8)
	mutated	75	(41.2)
	NA	0	(0)
BRAF	wild type	133	(73.1)
	mutated	13	(7.1)
	NA	36	(19.8)

Supplementary File 2E

Case_ID	Gender	DOB	Age	GE/ml (LINE1)	Plasma Date	DATE CEA	CEA	DELTA T CEA/BLOOD BRAW	TREATMENT	Start Treatment	Last administration (before Plasma Collecting)	No_current_treatment	DELTA BASELINE-PLASMA	PCR	TC Scan Date	DELTA BASELINE	TUMOR BURDEN RECIST (mm)	BULKY DISEASE	T IN SITU	N metastatic sites	LIVER	LUNG	NODES	PERITONEUM	BONE	OTHER SITES	KRAS	NRAS	KRAS+NRAS	BRAF
CRC_Monitoring_1	F	1-Jan-43	69.0	52861.4	9-Dec-11	9-Dec-11	100	0	Dacarbazina	10-Nov-11	30-Nov-11	0	-9	3	10-Nov-11	-29	158	0	0	3	1	1	0	1	0	0	1		1	0
CRC_Monitoring_2	F	17-Oct-34	76.1	60603.1	11-Nov-10	10-Nov-10	229.2	-1	PmAb	15-Sep-10	10-Nov-10	0	-1	2	16-Nov-10	5	92	0	0	2	0	0	0	0	1	1	0		0	0
CRC_Monitoring_3	F	4-Aug-67	47.2	26504.8	15-Oct-14	17-Sep-14	765.6	-28	MEK162	1-Oct-14	1-Oct-14	0	-14	2	17-Nov-14	33	115	1	0	2	1	0	1	0	0	0	0	0	0	0	0
CRC_Monitoring_4	M	5-Apr-45	69.4	35085.2	5-Aug-14	2-Jul-14	17.7	-34	no treatment			1		2	16-Jul-14	-20	104	1	0	2	0	1	1	0	0	0	0	1	1	0	0
CRC_Monitoring_5	F	25-Dec-66	48.3	35851.8	8-Apr-15	13-Apr-15	387.2	5	HERACLES	14-Apr-15	14-Apr-15	1	6	4	8-Apr-15	0	124	0	0	3	1	1	1	0	0	0	0		0	0	
CRC_Monitoring_6	M	25-Dec-44	64.8	30699.0	9-Sep-09	18-Sep-09	45.5	9	no treatment			1		4	16-Sep-09	7	193	0	0	4	1	0	1	0	0	2			0	0	
CRC_Monitoring_7	F	17-Aug-54	55.8	30438.3	4-May-10	3-May-10	3	-1	no treatment			1		2	4-Jun-10	31	65	1	0	3	1	0	1	0	0	1	0		0	0	0
CRC_Monitoring_8	M	7-Aug-29	83.0	201913.5	29-Jun-12	28-Jun-12	1738	-1	Folfiri+Beva	29-Jun-12	29-Jun-12	1	0	2	7-Jun-12	-22	109	0	0	1	1	0	0	0	0	0	0		0	0	0
CRC_Monitoring_9	M	31-Jul-47	64.0	88959.6	8-Jul-11	20-Jun-11	119.6	-18	Folfiri	21-May-11	20-Jun-11	0	-18	3	11-Jul-11	3	192	1	0	2	1	0	1	0	0	0	1		1	0	
CRC_Monitoring_10	M	28-Jan-46	68.8	204675.3	6-Nov-14	10-Nov-14	6.4	4	Folfiri	20-Oct-14	20-Oct-14	0	-17	0	7-Nov-14	1	86	0	0	3	1	0	1	0	0	1	0	0	0	0	1
CRC_Monitoring_11	M	6-Jul-58	56.9	196187.1	18-May-15	7-May-15	32.9	-11	ELO		18-Mar-15	1	-61	1	7-May-15	-11	31	0	0	1	1	0	0	0	0	0	0	0	0	0	0
CRC_Monitoring_12	M	9-Sep-44	71.2	84931.2	23-Oct-15	23-Oct-15	9.8	0	Folfo+Beva	9-Nov-15	2-Mar-15	1	-235	1	27-Oct-15	4	28	0	0	1	0	0	0	0	0	1	1		1	0	
CRC_Monitoring_13	M	23-Oct-60	51.0	449292.9	3-Oct-11	19-Sep-11	835.5	-14	GA201	10-Oct-11	15-Sep-11	0	-18	1	19-Sep-11	-14	122	1	1	2	1	0	1	0	0	0	0		0	0	
CRC_Monitoring_14	F	20-Mar-43	68.2	19396.6	25-May-11	25-May-11	60.5	0	PmAb	25-May-11	24-May-11	0	-1	2	15-Apr-11	-40	43	0	0	4	1	0	0	0	1	0	0		0	0	1
CRC_Monitoring_15	M	17-Apr-32	80.8	181456.6	7-Jan-13	7-Jan-13	2.6	0	PmAb	5-Dec-12	20-Dec-12	0	-18	3	28-Jan-13	21	35	0	0	2	0	1	0	0	0	0	0		0	0	
CRC_Monitoring_16	M	18-Feb-42	73.4	215847.9	2-Jul-15	8-Jul-15	1.1	6	PmAb+Tramet	16-Jul-15	16-Jul-15	1	14	3	9-Jul-15	7	12	0	0	2	0	1	0	0	0	0	0		0	0	1
CRC_Monitoring_17	M	26-Nov-40	69.6	10659.3	24-Jun-10	24-Jun-10	21	0	no treatment			1		1	3-May-10	-52	117	0	0	2	1	0	0	1	0	0	0		0	0	1
CRC_Monitoring_18	F	4-Oct-60	54.5	154841.2	8-Apr-15	8-Apr-15	9762	0	Irinotecan	1-Apr-15	1-Apr-15	0	-7	3	26-Mar-15	-13	226	1	1	3	1	1	0	0	0	0	0		0	0	
CRC_Monitoring_19	M	30-Nov-37	72.5	120155.3	25-May-10	23-Jun-10	8.7	29	Irinotecan	22-May-10	22-May-10	0	-3	0	4-May-10	-21	117	0	1	1	1	0	0	0	0	0	0		0	0	
CRC_Monitoring_20	M	3-Jul-62	49.6	47477.6	6-Feb-12	5-Dec-11	228.6	-63	Pre-Surgery - No treatment			1		1	1-Feb-12	-5	83	0	1	1	1	0	0	0	0	0	0		0	0	
CRC_Monitoring_21	M	25-May-39	74.5	131904.1	18-Nov-13	18-Nov-13	858.9	0	no treatment			1		3	18-Nov-13	0			1	2	1	1	0	0	0	0	1		1	0	
CRC_Monitoring_22	M	21-Jul-34	76.0	48021.2	20-Jul-10	19-Jul-10	27.7	-1	Folfo	14-May-10	19-Jul-10	0	-1	0	9-Aug-10	20	113	1	0	1	1	0	0	0	0	0	0		0	0	
CRC_Monitoring_23	F	11-Feb-41	70.0	95896.7	19-Jan-11	18-Jan-11	89.3	-1	Folfiri	15-Sep-10	18-Jan-11	0	-1	1	19-Apr-11	90	44	0	0	2	0	0	0	1	0	1	1		1	0	
CRC_Monitoring_24	M	24-Dec-58	56.8	21320.9	18-Sep-15	2-Sep-15	491.2	-16	PmAb+Tramet	4-Aug-15	4-Sep-15	0	-14	3	15-Oct-15	27	87	1	0	3	0	1	1	0	0	1	0		0	0	1
CRC_Monitoring_25	M	25-May-49	61.1	1294369.3	23-Jun-10	23-Jun-10	107.8	0	Folfo	23-Jun-10	23-Jun-10	1	0	0	4-Jun-10	-19	58	0	1	3	1	0	0	0	0	1	0		0	0	
CRC_Monitoring_26	M	11-Apr-41	69.6	157496.2	19-Oct-10	28-Sep-10	1.7	-21	Folfo+Cmab	6-Aug-10	28-Sep-10	0	-21	0	27-Oct-10	8			1	1	1	0	0	0	0	0	0		0	0	
CRC_Monitoring_27	F	13-Nov-34	79.8	272173.8	4-Aug-14	23-Jun-14	113.6	-42	Folfiri	14-May-14	22-Jul-14	0	-13	2	30-Jun-14	-35	84	0	1	3	1	1	0	0	1	0	1		1	0	
CRC_Monitoring_28	M	11-May-51	63.6	409422.1	20-Nov-14	20-Nov-14	7.3	0	Pre-Surgery - No treatment			1		1	21-Oct-14	-30	42	0	0	1	1	0	0	0	0	0	0		0	0	
CRC_Monitoring_29	F	28-Apr-40	74.2	288828.3	24-Jun-14	25-Jun-14	2.7	1	Folfo	20-May-14	23-Jun-14	0	-1	0	22-May-14	-33	167	0	0	3	0	0	1	1	0	1	0	0	0	1	
CRC_Monitoring_30	M	28-Nov-45	68.7	21913.7	1-Aug-14	24-Jun-14	67.4	-38	Folfiri	16-Jul-14	16-Jul-14	0	-16	1	30-Jun-14	-32	161	0	0	3	1	0	1	0	0	1	1	0	1	0	
CRC_Monitoring_31	F	12-Apr-64	49.8	214073.7	21-Jan-14	21-Jan-14	473.5	0	no treatment			1		3	15-Jan-14	-6			0	3	1	0	1	0	0	1	0		0	0	1
CRC_Monitoring_32	F	30-Jun-45	69.7	164095.6	11-Mar-15	8-Jan-15	5.5	-62	Pre-Surgery - No treatment			1		1	11-Mar-15	0	46	0	0	1	1	0	0	0	0	0	0	1	1	0	
CRC_Monitoring_33	M	16-Nov-35	78.7	176952.6	26-Jun-14	26-Jun-14	278.2	0	Pre-Surgery - No treatment			1		1	7-Apr-14	-80	43	0	0	1	1	0	0	0	0	0			0	0	
CRC_Monitoring_34	M	1-May-28	82.7	77612.2	21-Dec-10	24-Dec-10	4.3	3	Folfiri	11-Dec-10	11-Dec-10	0	-10	1	16-Dec-10	-5	57	0	1	1	1	0	0	0	0	0	1		1	0	
CRC_Monitoring_35	M	26-May-42	72.3	155034.4	3-Sep-14	8-Jul-14	24.2	-57	PmAb	11-Sep-14	9-Jul-14	1	-56	2	9-Sep-14	6	81	0	0	1	1	0	0	0	0	0	0	0	0	0	
CRC_Monitoring_36	F	19-Jul-40	73.8	485302.7	8-Apr-14	17-Mar-14	4189	-22	Folfo	23-Jan-14	7-Apr-14	0	-1	0	15-May-14	37	175	1	1	2	1	0	1	0	0	1	0	1	0	1	0
CRC_Monitoring_37	F	20-Dec-40	69.8	3718000.8	14-Sep-10	14-Sep-10	48.5	0	Mitomicina+5FU	14-Sep-10	4-Aug-10	1	-41	2	9-Aug-10	-36	61	0	0	2	1	0	0	0	0	0	1		1	0	
CRC_Monitoring_38	F	19-Jan-42	72.7	517187.6	10-Sep-14	26-Aug-14	4.8	-15	no treatment			1		0	10-Sep-14	0	19	0	1	1	1	0	0	0	0	0	0	0	0	0	
CRC_Monitoring_39	M	25-May-60	50.2	33734.4	28-Jul-10	13-Aug-10	3.3	16	PmAb	9-Apr-10	1-Jul-10	0	-27	2	8-Jul-10	-20	18	0	0	1	1	0	0	0	0	0	0		0	0	
CRC_Monitoring_40	M	29-Apr-44	70.0	10562.6	14-Apr-14	14-Apr-14	17.2	0	no treatment			1		3	2-Apr-14	-12	72	0	0	2	0	1	1	0	0	0			0	0	
CRC_Monitoring_41	M	20-Apr-48	67.0	6878.7	23-Mar-15	23-Mar-15	1.7	0	Pre-Surgery - No treatment			1		1	23-Mar-15	0	75	0	1	1	1	0	0	0	0	0			0	0	
CRC_Monitoring_42	M	30-Jun-40	72.5	25247.4	11-Dec-12	11-Dec-12	2	0	PmAb	14-Aug-12	27-Nov-12	0	-14	2	14-Dec-12	3	59	0	0	2	1	0	0	1	0	0	1		1	0	
CRC_Monitoring_43	M	26-Oct-36	79.0	167832.7	15-Oct-15	13-Oct-15	2	-2	Pre-Surgery - No treatment			1		0	15-Oct-15	0	25	0	0	1	1	0	0	0	0	0			0	0	
CRC_Monitoring_44	M	20-Apr-55	59.3	103753.4	5-Aug-14	5-Aug-14	8.6	0	no treatment			1		1	11-Sep-14	37	81	1	1	4	1	0	1	0	0	1	0	0	0	1	0
CRC_Monitoring_45	M	16-Jul-74	40.3	818211.6	5-Nov-14	5-Nov-14	1267	0	Pre-Surgery - No treatment			1		0	6-Nov-14	1	75	1	0	1	1	0	0	0	0	0			0	0	
CRC_Monitoring_46	M	1-Jun-29	81.0	96154.5	11-May-10	11-May-10	7.5	0	Folfo	9-May-10	9-May-10	0	-2	2	22-Apr-10	-19	41	0	0	1	0	0	1	0	0	0			0	0	
CRC_Monitoring_47	M	21-Dec-68	46.5	28029.4	10-Jun-15	10-Jun-15	31.4	0	no treatment			1		4	16-May-15	-25	110	1	0	1	1	0	0	0	0	0			0	0	
CRC_Monitoring_48	M	16-Jul-35	75.3	8874.5	12-Oct-10	9-Nov-10	27	28	Folfiri	3-Sep-10	24-Sep-10	0	-18	2	20-Jul-10	-84	10	0	0	1	0	0	0	0	0	1	0		0	0	
CRC_Monitoring_49	M	29-Nov-41	73.5	39603.6	8-May-15	20-Apr-15	12.1	-18	Folfo	21-Apr-15	20-Apr-15	0	-18	0	19-Jun-15	42	32	0	0	2	1	1	0	0	0	0	0	0	0	0	
CRC_Monitoring_50	F	11-Jul-56	58.1	83437.2	23-Jul-14	22-Jul-14	250	-1	Pre-Surgery - No treatment			1		0	23-Jul-14	0	55	0	1	1	1	0	0	0	0	0	1		1	0	
CRC_Monitoring_51	M	23-Sep-47	67.7	41904.5	8-May-15	8-May-15	71.7	0	no treatment			1		4	14-Apr-15	-24	200	0	0	3	1	1	1	0	0	0	0	0	0	0	
CRC_Monitoring_52	F	27-Nov-49	64.8	8307.2	2-Sep-14	14-Jul-14	13.6	-50	no treatment			1		3	18-Aug-14	-15	250	1	0	4	1	1	0	0	0	1	0	0	0	0	0
CRC_Monitoring_53	M	27-Mar-29	85.2	26651.3	30-May-14	30-May-14	147.3	0	PmAb	16-May-14	16-May-14	0	-14	2	9-May-14	-21	86.8	1	0	2	1	0	0	0	1	0	0	0	0	0	0
CRC_Monitoring_54	F	29-Mar-32	81.6	100139.2	3-Oct-13	11-Sep-13	8	-22	no treatment			1		0	12-Sep-13	-21	77	0	1	2	1	0	1	0	0	0			0	0	
CRC_Monitoring_55	M	28-May-52	61.1	1006748.2	5-Jun-13	4-Jun-13	418.7	-1	no treatment			1		6	16-May-13	-20			0	2	1	1	0	0	0	0	0		0	0	1
CRC_Monitoring_56	F	2-May-31	82.8	21946.5	27-Jan-14	27-Jan-14	193.6	0	PmAb	26-Nov-13	13-Jan-14	0	-14	0	10-Sep-13	-139	15	0	0	1	1	0	0	0	0	0	0		0	0	
CRC_Monitoring_57	F	19-Sep-74	40.1	31568.7	30-Oct-14	29-Oct-14	1085	-1	no treatment			1		2	31-Oct-14	1	141	1	0	1	1	0	0	0	0	0	1	0	1	0	
CRC_Monitoring_58	M	4-Oct-76	34.7	1572.9	8-Jun-11	7-Jun-11	20543	-1	no treatment			1		3	10-Jun-11	2	210	1	0	1	1	0	0	0	0	0	1		1	0	
CRC_Monitoring_59	M	23-May-33	80.6	12264.0	22-Nov-13	22-Nov-13	235.4	0	Folfiri+Cmab	22-Nov-13	6-Nov-13	0	-16	1	28-Nov-13	6	124	1	0	3	1	1	1	0	0	0	0		0	0	
CRC_Monitoring_60	M	10-Jul-49	63.8	220621.9	2-Apr-13	18-Mar-13	72.1	-15	Recourse	18-Mar-13	30-Mar-13	0	-3	4	18-Mar-13	-15	36	0	0	3	1	1	0	0	0	0	0		0	0	
CRC_Monitoring_61	F	9-Apr-51	60.6	12394.0	11-Nov-11	25-Oct-11	1084	-17	Folfo	26-Oct-11	26-Oct-11	0	-16	0	26-Sep-11	-46	152.5	0	1	2	1	0	1	0	0	0	1		1	0	
CRC_Monitoring_62	F	28-Oct-54	55.8	7130.7	22-Jul-10	8-Jul-10	10	-14	Cmab+CPT11	3-Feb-10	8-Jul-10	0	-14	1	19-Aug-10	28	60	1	0	2	1	0	0	1	0	1	0		0	0	
CRC_Monitoring_63	F	12-Feb-81	33.3	4692.3	4-Jun-14	4-Jun-14	918.4	0	no treatment			1		2	1-Apr-14	-64			0	3	1	1	1	0	0	0	1		1	0	
CRC_Monitoring_64	F	17-Nov-78	35.1	32810.7	23-Dec-13	25-Nov-13	54.4	-28	Dareck	18-Nov-13	13-Dec-13	0	-10	1	6-Nov-13	-47	35	0	0	2	0	1	0	1	0	0	0		0	0	
CRC_Monitoring_65	F	22-Dec-63	50.0	18510.0	29-Nov-13	25-Nov-13	8.7	-4	Lung metastasectomy			1		0	27-Nov-13	-2	20	0	0	1	0	1	0	0	0	0	1		1	0	
CRC_Monitoring_66	M	6-Apr-70	43.3	32359.9	8-Jul-13	8-Jul-13	102	0	CmAb+Folfiri	30-Apr-13	25-Jun-13	0	-13	2	28-Jun-13	-10	200	0	0	2	1	0	0	0	0	0	0		0	0	
CRC_Monitoring_67	F	11-Aug-62	52.5	1212.5	29-Jan-15	13-Mar-15	2	43	Pre-Surgery - No treatment			1		1	29-Dec-14	-31	20	0	0	2	1	0	1	0	0	0	0	1	1	0	
CRC_Monitoring_68	M	4-Nov-64	50.7	46937.4	15-Jul-15	15-Jul-15	39.9	0	no treatment			1		1	16-Jul-15	1	139	0	0	2	1	0	0	1	0	0	0		0	0	1
CRC_Monitoring_69	F	15-Aug-36	77.2	6438.8	1-Oct-13	9-Sep-13	156.5	-22	Irinotecan	25-May-13	19-Jul-13	1	-74	1	9-Sep-13	-22	122	0	0	3	1	0	0	1	1	0	0		0	0	
CRC_Monitoring_70	F	14-Nov-42	68.5	1193.6	20-Apr-11	20-Apr-11	8.9	0	no treatment			1		2	20-Apr-11	0			0	2	1	1	0	0	0	0	0		0	0	
CRC_Monitoring_71	M	30-Mar-41	72.7	547401.1	18-Nov-13	27-Sep-13	11.2	-52	Above	15-Apr-13	30-Sep-13	1	-49	0	18-Sep-13	-61	51	0	1	2	1	0	0	0	0	1	1	0	1	0	
CRC_Monitoring_72	F	30-Dec-73	38.1	20302.3	30-Jan-12	6-Mar-12	38.3	36	GA201	16-Dec-11	23-Jan-12	0	-7	2	14-Jan-12	-16	136	0	0	2	0	0	0	0	0	1	0		0	0	
CRC_Monitoring_73	M	21-Jan-59	55.6	93202.7	1-Aug-14	18-Jul-14	88.6	-14	Folfiri	21-Jul-14	21-Jul-14	0	-11	2	30-May-14	-63	45	0	0	1	1	0	0	0	0	0	0	0	0	0	
CRC_Monitoring_74	M	7-Dec-39	75.8	107551.8	2-Sep-15	2-Sep-15	43.7	0	no treatment			1		4	3-Sep-15	1	154	0	0	3	1	1	0	0	0	1		0	0		
CRC_Monitoring_75	M	27-Jul-50	65.4	7137.3	25-Nov-15	14-Dec-15	24.1	19	Folfo	15-Oct-15	19-Oct-15	1	-37	0	16-Oct-15	-40	32	0	0	1	1	0	0	1	0	0	0	0	0	0	
CRC_Monitoring_76	M	4-Jan-53	62.7	18897.8	19-Aug-15	19-Aug-15	46.4	0	SYM	23-Jul-15	13-Aug-15	0	-6	2	27-Aug-15	8	90	0	1	3	1	0	0	0	0	1	0	0	0	0	
CRC_Monitoring_77	M	21-Jun-44	66.1	211770.7	12-Jul-10	5-Jul-10	294.4	-7	CmAb+Lenalidomide	17-May-10	20-Mar-10	1	-114	4	9-Jul-10	-3	90	0	0	3	1	1	0	0	0	0	1		1	0	
CRC_Monitoring_78	M	16-Oct-56	58.2	286363.4	5-Dec-14	5-Dec-14	6.3	0	PmAb+Folfo	6-Oct-14	17-Nov-14	0	-18	0	26-Nov-14	-9			1	1	1	0	0	0	0	0	0	0	0	0	
CRC_Monitoring_79	F	22-Nov-60	51.7	1087810	26-Jul-12	15-Jun-12	339	-41	Folfo	23-Jun-12	24-Jul-12	0	-2	0	27-Jun-12	-29	78	1	1	2	1	0	1	0	0	0	0		0	0	1
CRC_Monitoring_80	M	13-Aug-62	50.9	12622.8	25-Jun-13	25-Jun-13	0.8	0	Folfiri+MEHD7945A	15-Mar-13	12-Jun-13	0	-13	0	10-Jun-13	-15	9	0	0	2	0	1	1	0	0	1	0		0	0	
CRC_Monitoring_81	F	16-Mar-57	53.3	25265.6	15-Jun-10	8-Jun-10	1184	-7	CmAb+Lenalidomide	25-May-10	8-Jun-10	0	-7	3	12-May-10	-34	99	1	0	3	1	1	1	0	0	0			0	0	

CRC_Monitoring_82	F	24-Oct-63	51.3	663475.4	9-Feb-15	9-Feb-15	3.3	0	PmAb+Folfo	13-Jan-15	27-Jan-15	0	-13	0	9-Jan-15	-31	90	0	1	3	1	0	1	0	0	1	0	0	0	0
CRC_Monitoring_83	M	15-Sep-63	49.6	58741.5	28-Mar-13	11-Feb-13	120.8	-45	CmAb+Irinotecan	28-Mar-13	9-Mar-13	0	-19	0	2-May-13	35	60	0	0	2	1	0	0	0	0	0	0		0	0
CRC_Monitoring_84	F	31-Jul-37	76.8	192324.6	18-Apr-14	24-Mar-14	7.5	-25	CmAb+Folfiri	3-Jan-14	8-Apr-14	0	-10	0	12-May-14	24	149	0	0	2	1	1	0	0	0	0	0	0	0	0
CRC_Monitoring_85	M	18-Feb-36	76.0	37876.5	30-Jan-12	30-Jan-12	63.5	0	Dacarbazina	9-Jan-12	9-Jan-12	0	-21	4	17-Dec-11	-44	107.3	0	0	4	1	1	1	1	0	0	1		1	0
CRC_Monitoring_86	M	8-May-54	57.6	279826.4	11-Nov-11	15-Nov-11	560.1	4	Dacarbazina	15-Nov-11	12-Oct-11	0	-30	6	14-Nov-11	3	153	1	0	3	1	1	1	0	0	0	0		0	
CRC_Monitoring_87	F	27-Nov-67	44.3	18227.6	15-Mar-12	15-Mar-12	1.1	0	Dacarbazina	15-Mar-12	15-Mar-12	1	0	6	15-Mar-12	0	38.4	0	0	1	0	0	1	0	0	0	0		0	
CRC_Monitoring_88	M	4-Nov-56	54.9	88515.9	31-Aug-11	25-Aug-11	11.4	-6	Dacarbazina	29-Aug-11	1-Jul-11	1	-61	4	26-Aug-11	-5	98.3	0	0	2	1	1	0	0	0	0	0		0	
CRC_Monitoring_89	F	23-Dec-35	75.7	48028.9	9-Aug-11	8-Aug-11	66.1	-1	Dacarbazina	9-Aug-11	15-Jun-11	1	-55	3	8-Aug-11	-1	75.9	0	0	2	1	0	1	0	0	0	1		1	0
CRC_Monitoring_90	M	27-Nov-44	67.2	31252.6	16-Jan-12	16-Jan-12	12.3	0	Dacarbazina	23-Jan-12	15-Oct-11	1	-93	3	26-Jan-12	10	97.1	0	0	2	1	0	1	0	0	0	0		0	
CRC_Monitoring_91	M	6-Apr-58	53.8	12879.9	9-Jan-12	9-Jan-12	161.9	0	Dacarbazina	12-Jan-12	15-Nov-11	1	-55	4	11-Jan-12	2	79.3	0	0	4	1	1	1	0	0	1	0		0	
CRC_Monitoring_92	F	14-Jul-36	75.1	44150.3	28-Jul-11	22-Aug-11	102.5	25	Dacarbazina	29-Jul-11	28-Jun-11	0	-30	3	28-Jul-11	0	64	0	0	1	0	0	1	0	0	0	1		1	0
CRC_Monitoring_93	M	5-Jan-38	74.0	16070.5	5-Dec-11	5-Dec-11	101.1	0	Dacarbazina	4-Oct-11	13-Nov-11	0	-22	4	3-Oct-11	-63	64	1	0	2	0	1	1	0	0	0	1		1	0
CRC_Monitoring_94	M	6-Sep-52	58.9	14936.5	15-Jul-11	15-Jul-11	30.3	0	Dacarbazina	15-Jul-11	10-Jun-11	1	-35	4	16-Jun-11	-29	39.5	0	0	2	1	1	0	0	0	0	1		1	0
CRC_Monitoring_95	F	19-May-55	56.1	168268.6	9-Jun-11	9-Jun-11	443.8	0	Dacarbazina	11-Jun-11	9-Feb-11	1	-120	4	10-Jun-11	1	29	1	0	2	1	1	0	0	0	0	0		0	
CRC_Monitoring_96	M	1-Jun-75	36.5	74046.0	5-Dec-11	5-Dec-11	2057	0	Dacarbazina	6-Dec-11	28-Oct-11	1	-38	2	6-Dec-11	1	93.2	1	0	1	1	0	0	0	0	0	0		0	0
CRC_Monitoring_97	M	30-Sep-41	70.1	124077.1	24-Oct-11	24-Oct-11	4.2	0	Dacarbazina	25-Oct-11	15-Aug-11	1	-70	4	24-Oct-11	0	63.1	1	0	2	1	1	0	0	0	0	1		1	0
CRC_Monitoring_98	F	5-Feb-52	59.9	20085.5	29-Nov-11	28-Nov-11	299.6	-1	Dacarbazina	29-Nov-11	3-Oct-11	1	-57	4	14-Nov-11	-15	69	0	0	1	0	1	0	0	0	0	0		0	
CRC_Monitoring_99	M	10-Apr-52	59.2	133205.0	8-Jun-11	8-Jun-11	9.7	0	Dacarbazina	9-Jun-11	15-Feb-11	1	-113	2	8-Jun-11	0	128	0	0	3	1	1	1	0	0	0	1		1	0
CRC_Monitoring_100	F	15-Jun-44	67.4	278709.5	5-Oct-11	3-Oct-11	868.5	-2	Dacarbazina	8-Oct-11	12-Sep-11	0	-23	3	4-Oct-11	-1	53.3	0	0	2	1	1	0	0	0	0	1		1	0
CRC_Monitoring_101	F	10-Apr-39	72.8	255619.6	23-Jan-12	23-Jan-12	26.1	0	Dacarbazina	24-Jan-12	16-Dec-11	1	-38	3	27-Dec-11	-27	181	1	0	2	1	1	0	0	0	0	0		0	0
CRC_Monitoring_102	M	25-Aug-34	77.1	108563.7	28-Sep-11	28-Sep-11	968.8	0	Dacarbazina	1-Oct-11	15-Jun-11	1	-105	5	29-Sep-11	1	125.6	1	0	2	1	1	0	0	0	0	0		0	
CRC_Monitoring_103	M	24-Jun-49	62.7	80164.5	14-Feb-12	14-Feb-12	241.5	0	Dacarbazina	14-Feb-12	13-Jan-12	1	-32	7	9-Feb-12	-5	191.9	0	0	2	1	1	0	0	0	0	0		0	
CRC_Monitoring_104	F	21-Apr-63	48.8	29126.1	10-Feb-12	10-Feb-12	186.5	0	Dacarbazina	27-Feb-12	20-Dec-11	1	-52	4	1-Feb-12	-9	160	0	0	4	1	1	1	0	0	1	0		0	
CRC_Monitoring_105	M	24-Aug-47	64.6	10282.6	14-Mar-12	14-Mar-12	12.7	0	Dacarbazina	27-Mar-12	15-Feb-12	0	-28	3	26-Mar-12	12	107.9	0	0	2	1	1	0	0	0	0	0		0	0
CRC_Monitoring_106	M	15-Jan-46	66.2	2046.3	12-Mar-12	12-Mar-12	155.4	0	Dacarbazina	20-Feb-12	20-Feb-12	0	-21	5	17-Feb-12	-24	112.8	1	0	2	1	1	0	0	0	0	0		0	
CRC_Monitoring_107	M	14-May-36	75.4	28040.5	5-Sep-11	5-Sep-11	60.2	0	Dacarbazina	6-Sep-11	11-Aug-11	0	-25	6	11-Aug-11	-25	112.6	0	0	2	0	1	0	0	0	1	1		1	0
CRC_Monitoring_108	M	23-Apr-53	58.4	12029.2	19-Aug-11	19-Aug-11	10.8	0	Dacarbazina	14-Jun-11	26-Jul-11	0	-24	2	12-Aug-11	-7	24	0	0	3	1	0	1	1	0	0	1		1	0
CRC_Monitoring_109	M	15-Mar-66	45.9	3700.3	30-Jan-12	30-Jan-12	231.9	0	Dacarbazina	31-Jan-12	19-Dec-11	1	-42	2	23-Jan-12	-7	97.9	1	0	2	1	1	0	0	0	0	0		0	
CRC_Monitoring_110	M	23-Apr-75	36.9	12044.0	20-Feb-12	20-Feb-12	569	0	Dacarbazina	21-Feb-12	15-Dec-11	1	-67	6	6-Feb-12	-14	174	1	0	3	1	0	1	0	0	1			0	
CRC_Monitoring_111	M	15-Oct-54	57.0	28588.4	19-Sep-11	25-Aug-11	3.3	-25	Dacarbazina	29-Aug-11	29-Aug-11	0	-21	2	4-Aug-11	-46	117.6	0	0	2	1	0	1	0	0	0	1		1	0
CRC_Monitoring_112	M	27-Sep-58	53.4	32088.4	26-Jan-12	25-Jan-12	78	-1	Dacarbazina	27-Jan-12	5-Dec-11	1	-52	5	26-Jan-12	0	55	1	0	2	1	1	0	0	0	0	1		1	0
CRC_Monitoring_113	F	16-Nov-41	70.1	97321.7	29-Nov-11	28-Nov-11	2930	-1	Dacarbazina	29-Nov-11	7-Nov-11	0	-22	3	7-Nov-11	-22	65.6	1	0	2	1	1	0	0	0	0	0		0	
CRC_Monitoring_114	M	30-Jan-39	72.7	27679.7	13-Sep-11	22-Aug-11	1.9	-22	Dacarbazina	11-Jul-11	23-Aug-11	0	-21	4	9-Sep-11	-4	65	0	0	1	0	1	0	0	0	0	1		1	0
CRC_Monitoring_115	F	9-Nov-69	41.9	266432.4	12-Sep-11	19-Aug-11	991.4	-24	Dacarbazina	28-Aug-11	23-Aug-11	0	-20	2													1		1	0
CRC_Monitoring_116	M	1-May-52	59.4	13431.5	2-Sep-11	19-Aug-11	45.2	-14	Dacarbazina	20-Jun-11	1-Aug-11	1	-32	3	5-Aug-11	-28	52.3	0	0	2	0	1	0	1	0	0	1		1	0
CRC_Monitoring_117	M	18-Aug-71	40.4	17440.7	17-Jan-12	17-Jan-12	44.8	0	Dacarbazina	23-Jan-12	15-Oct-11	1	-94	3	4-Jan-12	-13	70.3	0	0	2	1	0	1	0	0	0	1		1	0
CRC_Monitoring_118	M	17-Jun-57	54.6	1110.9	24-Jan-12	24-Jan-12	7.1	0	Dacarbazina	26-Jan-12	15-Dec-11	1	-40	5	26-Jan-12	2	55.5	0	0	1	0	0	0	1	0	0	1		1	0
CRC_Monitoring_119	M	15-Jul-30	81.0	350586.4	13-Jun-11	10-Jun-11	167.8	-3	Dacarbazina	11-Jun-11	11-Jun-11	0	-2	3	10-Jun-11	-3	113	0	0	2	0	1	1	0	0	0	1		1	0
CRC_Monitoring_120	M	6-Jan-35	76.9	51240.2	7-Nov-11	3-Nov-11	1600	-4	Dacarbazina	4-Nov-11	4-Nov-11	0	-3	4	3-Nov-11	-4	53.7	0	0	1	1	0	0	0	0	0	0		0	0
CRC_Monitoring_121	M	17-Jun-42	69.6	100424.6	23-Jan-12	23-Jan-12	69.3	0	Dacarbazina	24-Jan-12	12-Dec-11	1	-42	4	19-Jan-12	-4	82.1	0	0	1	1	0	0	0	0	0			0	
CRC_Monitoring_122	M	25-Feb-37	74.9	83442.6	15-Dec-11	12-Dec-11	282.2	-3	Dacarbazina	13-Dec-11	13-Dec-11	0	-2	3	29-Nov-11	-16	109.6	0	0	2	1	0	0	0	0	1	0		0	
CRC_Monitoring_123	M	9-Oct-37	74.2	9259907.7	14-Dec-11	18-Dec-11	34.1	4	Dacarbazina	15-Dec-11	15-Oct-11	1	-60	2	14-Dec-11	0	198	1	0	2	1	0	1	0	0	0	1		1	0
CRC_Monitoring_124	F	26-Nov-53	57.7	124284.9	8-Aug-11	4-Aug-11	82.9	-4	Dacarbazina	6-Aug-11	6-Aug-11	0	-2	4	5-Aug-11	-3	40.3	1	0	1	0	1	0	0	0	0	0		0	
CRC_Monitoring_125	F	11-Nov-40	70.7	152843.3	4-Jul-11	4-Jul-11	151.7	0	Dacarbazina	4-Jul-11	15-Mar-11	1	-111	4	1-Jul-11	-3	40	1	0	2	1	1	0	0	0	0	0		0	0
CRC_Monitoring_126	M	29-May-48	63.5	10694.6	7-Nov-11	4-Nov-11	4.4	-3	Dacarbazina	8-Nov-11	7-Oct-11	1	-31	3	7-Nov-11	0	62.6	0	0	2	0	1	0	1	0	0	1		1	0
CRC_Monitoring_127	M	9-Jun-38	73.5	39522.9	11-Nov-11	11-Nov-11	211.5	0	Dacarbazina	15-Nov-11	15-Oct-11	0	-27	2	14-Nov-11	3	91	0	0	2	1	0	1	0	0	0	1		1	0
CRC_Monitoring_128	F	19-Feb-44	67.6	325832.1	26-Sep-11	26-Sep-11	2581	0	Dacarbazina	26-Sep-11	15-Aug-11	1	-42	4	10-Nov-11	45	30	1	0	1	0	1	0	0	0	0	0		0	0
CRC_Monitoring_129	M	20-Oct-45	65.8	28485.4	20-Jul-11	18-Jul-11	246.4	-2	Dacarbazina	20-Jul-11	15-Jun-11	1	-35	6	19-Jul-11	-1	113.3	0	0	3	1	1	0	0	0	1	0		0	
CRC_Monitoring_130	F	5-May-71	40.8	2361.0	10-Feb-12	10-Feb-12	18.6	0	Dacarbazina	11-Feb-12	2-Dec-11	1	-70	4	10-Feb-12	0	49	0	0	2	0	1	0	0	0	1	1		1	0
CRC_Monitoring_131	M	9-Sep-42	69.0	8482.1	1-Sep-11	30-Aug-11	79.9	-2	Dacarbazina	6-Aug-11	30-Aug-11	0	-2	6	9-Aug-11	-23	37	1	0	2	0	1	1	0	0	0	0		0	
CRC_Monitoring_132	M	26-Aug-36	74.7	9992.4	3-May-11	4-May-11	5.3	1	PmAb	18-May-11	4-Apr-11	0	-29	2	4-Apr-11	-29	50	0	1	1	1	0	0	0	0	0			0	0
CRC_Monitoring_133	F	20-Sep-67	45.8	4188490	11-Jul-13	11-Jul-13	3321	0	PmAb	12-Jul-13	17-Apr-13	1	-85	4	27-Jun-13	-14	65	1	1	1	1	0	0	0	0	0		0	0	
CRC_Monitoring_134	M	28-Jun-59	52.7	2400999.3	16-Feb-12	16-Feb-12	8828	0	PmAb	16-Feb-12	27-Jan-12	0	-20	2	30-Jan-12	-17	123	0	1	1	1	0	0	0	0	0			0	0
CRC_Monitoring_135	M	21-Feb-41	70.5	24307	29-Jul-11	29-Jul-11	39.3	0	PmAb	2-Aug-11	20-Apr-11	1	-100	2	28-Jul-11	-1	105	0	0	2	1	1	0	0	0	0	0		0	0
CRC_Monitoring_136	M	8-Mar-54	59.0	51765	6-Mar-13	5-Mar-13	3.3	-1	PmAb	6-Mar-13	18-Dec-12	1	-78	2	1-Feb-13	-33	16	0	0	1	0	0	0	0	0	1		0	0	
CRC_Monitoring_137	F	15-Sep-64	45.9	28860.0	23-Jul-10	23-Jul-10	1.3	0	PmAb	29-Mar-13	15-Jul-10	0	-8	2	14-Jul-10	-9	39	0	0	1	0	0	1	0	0	0			0	0
CRC_Monitoring_138	M	27-Jun-30	82.9	49712	30-Apr-13	16-May-13	60.4	16	PmAb	2-May-13	27-Mar-13	1	-34	2	2-Apr-13	-28	86	0	0	2	1	0	1	0	0	0			0	0
CRC_Monitoring_139	M	12-Oct-38	74.7	24183	22-May-13	22-May-13	2.6	0	PmAb	23-May-13	8-Feb-13	1	-103	2	14-Mar-13	-69	88	0	0	3	1	1	1	0	0	0	0	0	0	0
CRC_Monitoring_140	M	19-May-48	68.1	101354.8	1-Jun-16	1-Jun-16	75.8	0	FOLFOX+Beva	3-Jun-16		1		0	18-May-16	-14	153	1	1	3	1	1	1	0	0	0	1		1	0
CRC_Monitoring_141	F	12-Oct-54	61.6	20210.3	19-Apr-16	11-May-16	56.3	22	Folfox+Beva	13-May-16		1		0	12-May-16	23	86	0	1	1	1	0	0	0	0	0	0		0	1
CRC_Monitoring_142	M	29-Apr-52	60.7	44483.9	28-Dec-12	28-Dec-12	137	0	TMZ	28-Dec-12	5-Dec-12	0	-23	5	4-Dec-12	-24	141	0	0	2	1	1	0	0	0	0	0		0	0
CRC_Monitoring_143	M	28-Mar-52	60.9	48356.6	25-Jan-13	24-Jan-13	44.5	-1	TMZ	26-Jan-13	15-Nov-12	1	-71	4	23-Jan-13	-2	117	0	0	3	1	1	1	0	0	0	1		1	0
CRC_Monitoring_144	M	1-Sep-59	54.0	17574.2	23-Aug-13	23-Aug-13	13.3	0	TMZ	27-Aug-13	5-Jul-13	1	-49	3	26-Aug-13	3	97	0	0	3	0	1	1	0	0	1	1		1	0
CRC_Monitoring_145	M	2-Aug-51	62.4	11773.6	19-Dec-13	19-Dec-13	80	0	TMZ	24-Dec-13	15-Nov-13	1	-34	2	20-Dec-13	1	84	0	0	3	0	1	1	0	0	1	1		1	0
CRC_Monitoring_146	F	3-Feb-41	72.5	19981.2	5-Jul-13	5-Jul-13	147.6	0	TMZ	12-Jul-13	19-Feb-13	1	-136	3	10-Jul-13	5	126	0	0	2	1	1	0	0	0	0	1		1	0
CRC_Monitoring_147	M	9-Mar-36	77.5	34425.0	3-Sep-13	3-Sep-13	138.2	0	TMZ	4-Sep-13	18-Jun-13	1	-77	2	23-Aug-13	-11	133	0	0	3	1	1	0	0	0	1	1		1	0
CRC_Monitoring_148	M	21-Feb-50	63.0	70062.1	21-Jan-13	21-Jan-13	3389	0	TMZ	29-Jan-13	15-Nov-12	1	-67	3	21-Jan-13	0	135.6	1	0	2	1	1	0	0	0	0	1		1	0
CRC_Monitoring_149	M	16-Dec-50	62.1	35596.9	14-Jan-13	29-Jan-13	2148	15	TMZ	16-Jan-13	16-Oct-12	1	-90	5	21-Dec-12	-24	167	0	0	3	0	1	1	0	0	1	0		0	0
CRC_Monitoring_150	M	23-Apr-51	62.0	21605.5	4-Apr-13	29-Mar-13	111.3	-6	TMZ	5-Apr-13	14-Feb-13	1	-49	2	4-Apr-13	0	84	1	0	2	0	1	1	0	0	0	1		1	0
CRC_Monitoring_151	F	19-Jan-68	45.3	19489.7	6-May-13	6-May-13	11.2	0	TMZ	13-May-13	8-Apr-13	0	-28	2	6-May-13	0	53	0	0	3	1	1	1	0	0	0	1		1	0
CRC_Monitoring_152	M	9-Feb-66	47.1	23568.1	14-Mar-13	11-Mar-13	19.2	-3	TMZ	27-Mar-13	15-Oct-12	1	-150	3	11-Mar-13	-3	34	0	0	2	0	1	0	0	0	1	0		0	0
CRC_Monitoring_153	M	12-May-72	40.9	14536.3	21-Mar-13	21-Mar-13	59.1	0	TMZ	25-Mar-13	28-Dec-12	1	-83	4	12-Mar-13	-9	57	0	0	4	1	1	1	0	0	1	1		1	0
CRC_Monitoring_154	F	4-Jul-56	56.6	40464.8	25-Jan-13	25-Jan-13	496.9	0	TMZ	29-Jan-13	15-Dec-12	1	-41	3	29-Jan-13	4	105.6	0	0	2	0	0	0	0	1	1	1		1	0
CRC_Monitoring_155	M	10-Jun-58	54.9	104241.0	3-Apr-13	11-Apr-13	634.7	8	TMZ	11-Apr-13	15-Feb-13	1	-47	2	8-Apr-13	5	107	1	0	3	1	1	1	0	0	0	0		0	
CRC_Monitoring_156	F	5-Mar-58	55.1	6089.3	10-Apr-13	10-Apr-13	68.4	0	TMZ	30-Apr-13	15-Jan-13	1	-85	3	12-Apr-13	2	29	0	0	1	0	1	0	0	0	0	0		0	0
CRC_Monitoring_157	F	24-Mar-49	64.1	18011.6	4-Apr-13	3-Apr-13	5	-1	TMZ	4-Apr-13	15-Dec-12	1	-110	5	18-Mar-13	-17	34.3	0	0	3	0	1	1	0	0	1	1		1	0
CRC_Monitoring_158	M	23-Mar-52	62.0	16364.5	28-Feb-14	27-Feb-14	6.8	-1	TMZ	2-Mar-14	15-Jan-14	1	-44	6	10-Feb-14	-18	29	0	0	1	1	0	0	0	0	0	0		0	0
CRC_Monitoring_159	M	7-Jan-58	56.0	32537.4	17-Dec-13	16-Dec-13	262.8	-1	TMZ	23-Dec-13	15-Jul-13	1	-155	3	18-Dec-13	1	172	1	0	3	1	1	0	0	0	1	1		1	0
CRC_Monitoring_160	M	25-Oct-40	73.4	23854.4	18-Feb-14	18-Feb-14	280	0	TMZ	21-Feb-14	15-Nov-13	1	-95	3	5-Feb-14	-13	107	1	0	2	1	1	0	0	0	0	0		0	1
CRC_Monitoring_161	F	8-Mar-46	68.0	28576.9	4-Mar-14	5-Mar-14	22	1	TMZ	6-Mar-14	14-Nov-13	1	-110	3	26-Feb-14	-6	29	0	0	1	0	1	0	0	0	0	0		0	0
CRC_Monitoring_162	F	10-May-53	60.1	35053.0	30-May-13	30-May-13	7.6	0	TMZ	31-May-13	30-Apr-13	0	-30	2	2-May-13	-28	79	0	0	2	1	1	0	0	0	0	1		1	0
CRC_Monitoring_163	M	27-May-47	65.8	40107.0	14-Feb-13	14-Feb-13	1.4	0	TMZ	18-Feb-13	17-Dec-12	1	-59	8	23-Jan-13	-22	190	1	0	3	1	1	0	0	0	1	1		1	0
CRC_Monitoring_164	F	20-Jan-60	53.1	75477.5	18-Feb-13	18-Feb-13	517.2	0	TMZ	22-Feb-13	18-Jan-13	1	-31	3	18-Feb-13	0	142	0	0	2	1	0	1	0	0	0	1		1	0
CRC_Monitoring_165	F	10-Jul-53	60.9	149958.5	14-May-14	30-Apr-14	274.2	-14	TMZ	15-May-14	15-Apr-14	0	-29	3	14-May-14	0	147	1	0	2	1	1	0	0	0	0	0		0	0
CRC_Monitoring_166	M	18-May-74	39.0	28811.0	14-May-13	14-May-13	57.5	0	TMZ	24-May-13	12-Mar-13	1	-63	3	23-May-13	9	48	0	1	3	1	1	1	0	0	0	0		0	0
CRC_Monitoring_167	M	27-Jun-60	53.0	13968.2	28-May-13	28-May-13	73	0	TMZ	31-May-13	15-Mar-13	1	-74	2	28-May-13	0	38	0	0	1	0	1	0	0	0	0	1		1	0
CRC_Monitoring_168	M	18-Nov-42	71.3	1210352.6	3-Mar-14	3-Mar-14	421.4	0	TMZ	6-Mar-14	1-Feb-14	0	-30	3	5-Feb-14	-26	85	1	0	2	1	1	0	0	0	0	1		1	0
CRC_Monitoring_169	M	1-Oct-50	63.0	306597.5	2-Oct-13	2-Oct-13	342.8	0	TMZ	10-Oct-13	14-Aug-13	1	-49	5	4-Oct-13	2	108	0	0	2	1	0	1	0	0	0	1		1	0
CRC_Monitoring_170	M	25-Dec-39	74.0	29332.6	19-Dec-13	16-Dec-13	51.6	-3	TMZ	20-Dec-13	5-Sep-13	1	-105	4	25-Nov-13	-24	69.2	0	0	2	0	1	1	0	0	0	0		0	0
CRC_Monitoring_171	M	3-Mar-48	65.4	100149.0	28-Jun-13	30-Jun-13	82.9	2	no treatment	28-Jun-13		1		0	8-May-13	-51	70	0	0	2	1	1					1		1	0
CRC_Monitoring_172	F	26-Oct-48	64.9	162360.0	19-Sep-13	19-Sep-13	78	0	no treatment	19-Sep-13		1		0	22-Jul-13	-59	113	0	1	2	1	1					1		1	0
CRC_Monitoring_173	F	1-Nov-37	76.0	37908.0	2-Oct-13	16-Sep-13	2.3	-16	no treatment	2-Oct-13		1		0	2-Aug-13	-61	40		0								1		1	0

CRC_Monitoring_174	M	17-Mar-44	70.0	9661.0	10-Feb-14	24-Oct-13	49.8	-109	no treatment	10-Feb-14		1		0	29-Oct-13	-104	47		0							1		1	0
CRC_Monitoring_175	F	13-Aug-47	66.8	341927.0	29-Apr-14	29-Apr-14	79	0	no treatment	29-Apr-14		1		0	4-Apr-14	-25	182		1	4	1	1	1		1	1		1	0
CRC_Monitoring_176	F	25-Jun-68	45.9	7014008.0	12-May-14	26-May-14	518.3	14	no treatment	12-May-14		1		0	14-Apr-14	-28	70	0	1	2	1		1			1		1	0
CRC_Monitoring_177	M	22-May-37	77.0	29728.0	13-May-14	13-May-14	455.9	0	no treatment	13-May-14		1		0	17-Apr-14	-26	110	0	0	4		1	1	1		1	1		1	0
CRC_Monitoring_178	F	5-Mar-52	61.4	95599.0	2-Jul-13	2-Jul-13	527	0	no treatment	2-Jul-13		1		0	20-Jun-13	-12	70		1							1		1	0
CRC_Monitoring_179	M	25-Jan-59	54.5	21720.0	3-Jul-13	23-May-13	1.8	-41	no treatment	3-Jul-13		1		0	20-May-13	-44	50		0							1		1	0
CRC_Monitoring_180	F	8-Apr-45	68.3	69420.0	15-Jul-13	15-Jul-13	28.9	0	no treatment	15-Jul-13		1		0	23-May-13	-53	70	0	0	1	1					1		1	0
CRC_Monitoring_181	M	12-Apr-52	64.0	13540.4	12-Apr-16				Folfox+Beva	3-May-16		1		0	11-Apr-16	-1	35	0	0	3	1		1	1		1		1	0
CRC_Monitoring_182	M	11-Dec-40	75.5	5980.8	19-May-16	4-May-16	2.8	-15	Folfox+Beva	5-May-16		0	-14	0	4-May-16	-15	56	0	0	2	1	1				1		1	0

Supplementary File 2F

Tissue_ID	Tissue Cohort	Concordance_Plasma	Tumor Extension	Average CH3		EYA4_%_1	unmethylated_events_1	methylated_events_1	EYA4_%_2	unmethylated_events_2	methylated_events_2	average_EYA4	STDEV_EYA4
Normal_Tissue_01	Matched Normal/Tumor Tissue Cohort			1.02	N	0.05	16493	9	0.40	12629	51	0.23	0.25
Tumor_Tissue_01	Matched Normal/Tumor Tissue Cohort			30.25	T	2.94	9248	280	12.41	9263	1312	7.68	6.70
Normal_Tissue_02	Matched Normal/Tumor Tissue Cohort			8.43	N	1.84	15811	297	1.93	13907	274	1.89	0.06
Tumor_Tissue_02	Matched Normal/Tumor Tissue Cohort			50.89	T	59.42	5802	8496	55.76	8596	10836	57.59	2.59
Normal_Tissue_03	Matched Normal/Tumor Tissue Cohort			1.77	N	0.29	22156	65	0.28	18236	51	0.29	0.01
Tumor_Tissue_03	Matched Normal/Tumor Tissue Cohort			33.97	T	31.86	15986	7476	16.22	12972	2512	24.04	11.06
Normal_Tissue_04	Matched Normal/Tumor Tissue Cohort			1.95	N	0.01	72740	7	0.01	103932	10	0.01	0.00
Tumor_Tissue_04	Matched Normal/Tumor Tissue Cohort			70.29	T	77.10	4913	16540	71.33	3786	9418	74.22	4.08
Normal_Tissue_05	Matched Normal/Tumor Tissue Cohort			6.71	N	1.64	38556	642	2.15	35056	769	1.90	0.36
Tumor_Tissue_05	Matched Normal/Tumor Tissue Cohort			88.62	T	82.10	4067	18655	81.60	4307	19106	81.85	0.35
Normal_Tissue_06	Matched Normal/Tumor Tissue Cohort			5.15	N	0.50	60788	305	0.54	54522	297	0.52	0.03
Tumor_Tissue_06	Matched Normal/Tumor Tissue Cohort			71.44	T	48.33	6066	5675	69.58	7738	17699	58.96	15.03
Normal_Tissue_07	Matched Normal/Tumor Tissue Cohort			7.39	N	0.54	46421	252	0.71	48864	347	0.63	0.12
Tumor_Tissue_07	Matched Normal/Tumor Tissue Cohort			36.60	T	0.17	64439	108	0.13	65699	86	0.15	0.03
Normal_Tissue_08	Matched Normal/Tumor Tissue Cohort			0.87	N	3.15	13758	447	2.24	45652	1044	2.70	0.64
Tumor_Tissue_08	Matched Normal/Tumor Tissue Cohort			58.85	T	55.99	4806	6114	41.91	6492	4683	48.95	9.96
Normal_Tissue_09	Matched Normal/Tumor Tissue Cohort			2.18	N	0.08	90345	74	0.09	89095	81	0.09	0.01
Tumor_Tissue_09	Matched Normal/Tumor Tissue Cohort			22.97	T	16.26	7476	1452	7.51	15864	1289	11.89	6.19
Normal_Tissue_10	Matched Normal/Tumor Tissue Cohort			2.18	N	0.50	46606	234	1.41	34350	490	0.96	0.64
Tumor_Tissue_10	Matched Normal/Tumor Tissue Cohort			83.23	T	60.01	6586	9882	78.26	4674	16821	69.14	12.90
Normal_Tissue_11	Matched Normal/Tumor Tissue Cohort			1.55	N	0.95	36001	344	0.19	20282	38	0.57	0.54
Tumor_Tissue_11	Matched Normal/Tumor Tissue Cohort			86.77	T	61.10	6325	9933	67.45	7172	14864	64.28	4.49
Normal_Tissue_12	Matched Normal/Tumor Tissue Cohort			0.77	N	0.18	6150	11	1.11	17453	196	0.65	0.66
Tumor_Tissue_12	Matched Normal/Tumor Tissue Cohort			90.03	T	67.69	5322	11148	79.25	3000	11459	73.47	8.17
Normal_Tissue_13	Matched Normal/Tumor Tissue Cohort			0.97	N	0.97	31267	305	0.41	59230	246	0.69	0.40
Tumor_Tissue_13	Matched Normal/Tumor Tissue Cohort			42.21	T	17.17	1548	321	29.57	7493	3146	23.37	8.77
Normal_Tissue_14	Matched Normal/Tumor Tissue Cohort			2.08	N	0.26	39826	1	0.28	21289	60	0.27	0.01
Tumor_Tissue_14	Matched Normal/Tumor Tissue Cohort			25.57	T	2.29	14454	338	4.68	18721	919	3.49	1.69
Normal_Tissue_15	Matched Normal/Tumor Tissue Cohort			4.06	N	0.60	28238	170	0.40	42789	173	0.50	0.14
Tumor_Tissue_15	Matched Normal/Tumor Tissue Cohort			63.60	T	22.93	4382	1304	19.49	6623	1603	21.21	2.43
Normal_Tissue_16	Matched Normal/Tumor Tissue Cohort			0.16	N	0.04	9850	4	0.01	14401	1	0.03	0.02
Tumor_Tissue_16	Matched Normal/Tumor Tissue Cohort			66.96	T	66.21	6023	11802	50.52	8385	8560	58.37	11.09
Normal_Tissue_17	Matched Normal/Tumor Tissue Cohort			2.37	N	0.99	22494	224	0.70	16780	118	0.85	0.21
Tumor_Tissue_17	Matched Normal/Tumor Tissue Cohort			46.11	T	52.53	3870	4283	41.95	4579	3309	47.24	7.48
Normal_Tissue_18	Matched Normal/Tumor Tissue Cohort			1.17	N	0.74	12544	93	0.61	19647	121	0.68	0.09
Tumor_Tissue_18	Matched Normal/Tumor Tissue Cohort			58.49	T	72.70	3401	9055	70.56	6311	15125	71.63	1.51
Normal_Tissue_19	Matched Normal/Tumor Tissue Cohort			2.28	N	0.29	65358	189	0.10	42991	42	0.20	0.13
Tumor_Tissue_19	Matched Normal/Tumor Tissue Cohort			20.17	T	14.39	20830	3500	9.79	20804	2257	12.09	3.25
Normal_Tissue_20	Matched Normal/Tumor Tissue Cohort			0.37	N	0.01	95626	11	0.02	71449	17	0.02	0.01
Tumor_Tissue_20	Matched Normal/Tumor Tissue Cohort			62.54	T	62.37	8062	13364	60.52	8738	13394	61.45	1.31
Normal_Tissue_21	Matched Normal/Tumor Tissue Cohort			0.34	N	1.14	49922	574	0.25	41484	105	0.70	0.63
Tumor_Tissue_21	Matched Normal/Tumor Tissue Cohort			32.89	T	22.23	10832	3096	17.89	20241	4409	20.06	3.07
Normal_Tissue_22	Matched Normal/Tumor Tissue Cohort			2.18	N	0.54	13662	74	0.94	16394	155	0.74	0.28
Tumor_Tissue_22	Matched Normal/Tumor Tissue Cohort			23.07	T	7.94	15323	1322	14.00	15384	2504	10.97	4.29
Normal_Tissue_23	Matched Normal/Tumor Tissue Cohort			5.40	N	0.19	12103	23	0.34	23271	79	0.27	0.11
Tumor_Tissue_23	Matched Normal/Tumor Tissue Cohort			67.66	T	28.69	8311	3343	34.96	7705	4142	31.83	4.43
Normal_Tissue_24	Matched Normal/Tumor Tissue Cohort			0.69	N	0.45	24970	113	0.53	13481	72	0.49	0.06
Tumor_Tissue_24	Matched Normal/Tumor Tissue Cohort			86.23	T	76.03	3379	10716	76.55	4216	13762	76.29	0.37
Normal_Tissue_25	Matched Normal/Tumor Tissue Cohort			0.65	N	0.40	28651	115	1.24	32851	414	0.82	0.59
Tumor_Tissue_25	Matched Normal/Tumor Tissue Cohort			58.75	T	37.39	5884	3514	40.63	10160	6953	39.01	2.29
Normal_Tissue_26	Matched Normal/Tumor Tissue Cohort			1.08	N	0.05	69572	38	0.13	68751	92	0.09	0.06
Tumor_Tissue_26	Matched Normal/Tumor Tissue Cohort			45.31	T	22.57	18902	5510	8.49	16982	1575	15.53	9.96
Normal_Tissue_27	Matched Normal/Tumor Tissue Cohort			3.23	N	0.64	41935	271	0.02	50133	10	0.33	0.44
Tumor_Tissue_27	Matched Normal/Tumor Tissue Cohort			25.27	T	18.68	9409	2162	13.55	9547	1497	16.12	3.63
Normal_Tissue_28	Matched Normal/Tumor Tissue Cohort			1.51	N	2.31	31867	755	0.78	34142	268	1.55	1.08
Tumor_Tissue_28	Matched Normal/Tumor Tissue Cohort			94.90	T	93.02	2604	34678	90.76	4130	40590	91.89	1.60
Normal_Tissue_29	Matched Normal/Tumor Tissue Cohort			2.29	N	0.38	34511	133	0.36	41635	151	0.37	0.01
Tumor_Tissue_29	Matched Normal/Tumor Tissue Cohort			74.76	T	85.24	3843	22190	93.04	2286	30553	89.14	5.52
Normal_Tissue_30	Matched Normal/Tumor Tissue Cohort			0.34	N	0.27	13919	38	0.06	9617	6	0.17	0.15
Tumor_Tissue_30	Matched Normal/Tumor Tissue Cohort			31.05	T	1.79	27615	504	2.20	26748	603	2.00	0.29
Normal_Tissue_31	Matched Normal/Tumor Tissue Cohort			1.16	N	0.64	34517	224	0.57	28973	166	0.61	0.05
Tumor_Tissue_31	Matched Normal/Tumor Tissue Cohort			62.03	T	45.40	7587	6308	45.62	7857	6590	45.51	0.16

Tissue_ID	GRIA4_%_1	unmethylated_events_1	methylated_events_1	GRIA4_%_2	unmethylated_events_2	methylated_events_2	average_GRIA4	STDEV_GRIA4	ITGA4_%_1	unmethylated_events_1	methylated_events_1	ITGA4_%_2	unmethylated_events_2	methylated_events_2	average_ITGA4	STDEV_ITGA4
Normal_Tissue_01	5.66	21551	1294	3.97	11642	481	4.82	1.20	0.00	998	0	0.04	2433	1	0.02	0.03
Tumor_Tissue_01	47.37	7045	6341	41.10	6385	4456	44.24	4.43	6.51	2068	144	8.92	643	63	7.72	1.70
Normal_Tissue_02	18.44	4759	1076	17.88	17953	3908	18.16	0.40	8.30	4760	431	8.95	12349	1214	8.63	0.46
Tumor_Tissue_02	45.64	2126	1785	49.17	11865	11478	47.41	2.50	55.66	4810	6038	54.51	3278	3928	55.09	0.81
Normal_Tissue_03	6.76	20372	1476	9.72	8050	867	8.24	2.09	0.13	7640	10	0.31	1907	6	0.22	0.13
Tumor_Tissue_03	55.65	5038	6322	63.49	6229	10833	59.57	5.54	40.43	1292	877	42.51	11598	8577	41.47	1.47
Normal_Tissue_04	9.83	3633	396	7.22	17755	1382	8.53	1.85	0.19	2588	5	0.14	10767	15	0.17	0.04
Tumor_Tissue_04	95.72	356	7954	92.46	1294	15866	94.09	2.31	93.55	1163	16865	92.92	546	7166	93.24	0.45
Normal_Tissue_05	24.15	6434	2049	24.82	16844	5562	24.49	0.47	0.61	7450	46	1.18	2420	29	0.90	0.40
Tumor_Tissue_05	92.08	858	9972	90.23	1512	13968	91.16	1.31	88.78	820	6486	91.30	1049	11005	90.04	1.78
Normal_Tissue_06	22.28	7479	2144	22.07	2231	632	22.18	0.15	0.64	8048	52	0.31	32877	101	0.48	0.23
Tumor_Tissue_06	81.60	1735	7693	84.26	2872	15378	82.93	1.88	74.70	4519	13345	71.18	1090	2692	72.94	2.49
Normal_Tissue_07	28.22	7096	2790	27.75	11975	4599	27.99	0.33	0.75	21846	165	0.69	4890	34	0.72	0.04
Tumor_Tissue_07	74.37	3722	10802	70.67	4515	10881	72.52	2.62	36.94	7975	4672	30.69	4412	1954	33.82	4.42
Normal_Tissue_08	2.26	260	6	0.23	3438	8	1.25	1.44	0.28	7860	22	0.28	2118	6	0.28	0.00
Tumor_Tissue_08	80.06	1283	5151	91.24	273	2843	85.65	7.91	28.60	252	101	25.24	3350	1131	26.92	2.38
Normal_Tissue_09	2.40	17590	433	8.77	16059	1543	5.59	4.50	0.11	28058	32	0.22	16886	37	0.17	0.08
Tumor_Tissue_09	43.09	8463	6407	17.13	8101	1675	30.11	18.36	20.35	8779	2243	18.05	5471	1205	19.20	1.63
Normal_Tissue_10	11.71	5784	767	6.53	24548	1716	9.12	3.66	0.16	22096	35	0.13	6373	8	0.15	0.02
Tumor_Tissue_10	87.93	835	6082	94.45	957	16291	91.19	4.61	84.28	2242	12019	80.70	493	2062	82.49	2.53
Normal_Tissue_11	2.05	9579	200	2.28	5315	124	2.17	0.16	0.43	21297	92	0.76	3265	25	0.60	0.23
Tumor_Tissue_11	90.53	1563	14945	89.14	2438	20007	89.84	0.98	91.43	578	6170	90.92	370	3705	91.18	0.36
Normal_Tissue_12	0.18	10134	18	0.42	15933	68	0.30	0.17	0.27	7682	21	0.33	5123	17	0.30	0.04
Tumor_Tissue_12	96.00	706	16946	98.81	229	19095	97.41	1.99	85.63	853	5082	84.53	975	5327	85.08	0.78
Normal_Tissue_13	1.03	6270	65	4.86	11632	594	2.95	2.71	0.23	23291	53	0.18	18749	34	0.21	0.04
Tumor_Tissue_13	79.49	1342	5202	73.26	3914	10724	76.38	4.41	39.73	176	116	31.56	4532	2090	35.65	5.78
Normal_Tissue_14	12.15	3686	510	7.16	8692	670	9.66	3.53	0.27	2927	8	0.09	8063	7	0.18	0.13
Tumor_Tissue_14	29.71	951	402	30.59	615	271	30.15	0.62	2.00	11248	230	2.79	2858	82	2.40	0.56
Normal_Tissue_15	17.86	2368	515	17.26	14716	3070	17.56	0.42	0.25	22469	57	0.30	7578	23	0.28	0.04
Tumor_Tissue_15	96.10	915	22518	86.53	1524	9791	91.32	6.77	30.19	481	208	36.71	967	561	33.45	4.61
Normal_Tissue_16	0.00	783	0	0.00	253	0	0.00	0.00	0.10	5167	5	0.31	1904	6	0.21	0.15
Tumor_Tissue_16	90.41	73	688	89.42	598	5053	89.92	0.70	57.59	687	933	59.09	369	533	58.34	1.06
Normal_Tissue_17	12.44	18003	2558	7.98	22901	1987	10.21	3.15	0.51	8507	44	0.09	9748	9	0.30	0.30
Tumor_Tissue_17	57.28	1742	2336	54.40	3245	3871	55.84	2.04	37.76	244	148	26.53	3598	1299	32.15	7.94
Normal_Tissue_18	0.11	10149	11	8.29	7425	671	4.20	5.78	0.29	6563	19	0.93	3515	33	0.61	0.45
Tumor_Tissue_18	63.26	907	1562	68.74	562	1236	66.00	3.87	63.49	2996	5211	70.76	2625	6351	67.13	5.14
Normal_Tissue_19	2.87	10045	297	18.59	10323	2358	10.73	11.12	0.00	1567	0	0.06	9334	6	0.03	0.04
Tumor_Tissue_19	19.91	3186	792	16.71	11651	2337	18.31	2.26	13.45	7124	1107	11.58	9894	1296	12.52	1.32
Normal_Tissue_20	0.00	8613	0	2.08	19674	417	1.04	1.47	0.20	16785	34	0.11	6328	7	0.16	0.06
Tumor_Tissue_20	77.05	767	2575	78.41	3108	11287	77.73	0.96	58.74	1612	2295	59.20	2930	4251	58.97	0.33
Normal_Tissue_21	0.70	1133	8	0.64	621	4	0.67	0.04	0.10	19460	19	0.05	2008	1	0.08	0.04
Tumor_Tissue_21	55.61	1666	2087	49.51	2944	2887	52.56	4.31	8.65	7644	724	9.41	16666	1731	9.03	0.54
Normal_Tissue_22	5.03	13467	714	14.52	1124	191	9.78	6.71	0.06	3218	2	0.08	4916	4	0.07	0.01
Tumor_Tissue_22	32.67	8764	4252	32.62	10186	4932	32.65	0.04	18.57	10661	2431	14.44	6917	1167	16.51	2.92
Normal_Tissue_23	19.21	8154	1939	20.20	20214	5116	19.71	0.70	0.08	4780	4	0.12	4189	5	0.10	0.03
Tumor_Tissue_23	75.90	2070	6518	64.91	3582	6625	70.41	7.77	70.47	686	1637	68.55	522	1138	69.51	1.36
Normal_Tissue_24	0.50	38683	194	3.55	15016	552	2.03	2.16	0.07	5372	4	0.34	4063	14	0.21	0.19
Tumor_Tissue_24	84.95	1710	9652	84.78	2297	12794	84.87	0.12	86.85	1910	12610	88.53	1026	7916	87.69	1.19
Normal_Tissue_25	0.48	24749	119	0.68	10077	69	0.58	0.14	0.11	35942	38	0.09	26736	24	0.10	0.01
Tumor_Tissue_25	82.31	2331	10844	77.03	2871	9627	79.67	3.73	83.34	1197	5988	81.25	568	2461	82.30	1.48
Normal_Tissue_26	4.85	6046	308	5.30	26842	1503	5.08	0.32	0.33	6040	20	0.07	6962	5	0.20	0.18
Tumor_Tissue_26	47.62	3650	3318	51.53	9624	10230	49.58	2.76	38.02	1901	1166	38.15	5927	3656	38.09	0.09
Normal_Tissue_27	13.38	2220	343	12.08	9542	1311	12.73	0.92	0.21	17788	38	0.32	25658	83	0.27	0.08
Tumor_Tissue_27	18.26	10231	2285	16.76	8925	1797	17.51	1.06	16.00	10327	1967	16.73	6875	1381	16.37	0.52
Normal_Tissue_28	0.64	4007	26	1.24	28825	362	0.94	0.42	0.35	24849	87	0.21	19734	41	0.28	0.10
Tumor_Tissue_28	95.18	434	8574	96.44	953	25812	95.81	0.89	97.32	1017	36998	95.05	390	7482	96.19	1.61
Normal_Tissue_29	1.96	13142	263	0.82	19058	157	1.39	0.81	0.26	38403	100	0.25	16088	41	0.26	0.01
Tumor_Tissue_29	95.12	544	10600	96.11	480	11850	95.62	0.70	92.30	1192	14289	88.25	422	3171	90.28	2.86
Normal_Tissue_30	0.47	34496	164	0.69	29937	208	0.58	0.16	0.89	1007	9	0.07	8219	6	0.48	0.58
Tumor_Tissue_30	46.44	4127	3579	37.13	2274	1343	41.79	6.58	34.47	1458	767	24.20	8030	2564	29.34	7.26
Normal_Tissue_31	1.91	9792	191	3.21	5600	186	2.56	0.92	0.56	23521	133	0.21	17925	38	0.39	0.25
Tumor_Tissue_31	72.36	4641	12149	65.98	6899	13378	69.17	4.51	69.52	4660	10630	62.79	3864	6519	66.16	4.76

Tissue_ID	MAP3K14-AS1_%_1	unmethylated_events_1	methylated_events_1	MAP3K14-AS1_%_2	unmethylated_events_2	methylated_events_2	average_MAP3K14-AS1	STDEV_MAP3K14-AS1	MSC_%_1	unmethylated_events_1	methylated_events_1	MSC_%_2	unmethylated_events_2	methylated_events_2	average_MSC	STDEV_MSC
Normal_Tissue_01	0.01	37353	4	0.00	46909	0	0.01	0.01	0.02	5723	1	0.00	25475	0	0.01	0.01
Tumor_Tissue_01	40.22	5640	3794	33.23	3980	1981	36.73	4.94	46.90	6655	5877	62.93	999	1696	54.92	11.33
Normal_Tissue_02	0.75	18847	142	1.83	14964	279	1.29	0.76	18.81	9949	2305	5.60	1398	83	12.21	9.34
Tumor_Tissue_02	21.76	9262	2576	28.29	5451	2150	25.03	4.62	68.95	2308	5126	69.74	1541	3552	69.35	0.56
Normal_Tissue_03	0.12	27927	34	0.12	28297	33	0.12	0.00	0.00	1041	0	0.00	4965	0	0.00	0.00
Tumor_Tissue_03	0.04	29092	11	0.03	46836	12	0.04	0.01	44.35	1246	993	45.09	2683	2203	44.72	0.52
Normal_Tissue_04	0.11	32980	36	0.14	24289	33	0.13	0.02	0.63	25527	161	1.18	16528	197	0.91	0.39
Tumor_Tissue_04	0.07	12764	9	0.01	18378	1	0.04	0.04	88.90	1340	10732	90.82	948	9374	89.86	1.36
Normal_Tissue_05	0.23	20885	48	0.26	16837	44	0.25	0.02	3.48	23600	852	8.61	6900	650	6.05	3.63
Tumor_Tissue_05	86.96	1386	9242	89.30	1654	13803	88.13	1.65	93.34	1498	20989	90.48	1804	17147	91.91	2.02
Normal_Tissue_06	0.12	28916	34	0.14	30823	42	0.13	0.01	3.49	5054	183	1.37	2086	29	2.43	1.50
Tumor_Tissue_06	57.76	2298	3142	64.44	3974	7202	61.10	4.72	81.99	1510	6875	80.55	3391	14047	81.27	1.02
Normal_Tissue_07	0.06	31284	20	0.24	10991	26	0.15	0.13	1.62	19979	330	13.30	5934	910	7.46	8.26
Tumor_Tissue_07	16.50	7549	1492	21.34	5040	1367	18.92	3.42	60.75	2156	3337	54.43	3033	3622	57.59	4.47
Normal_Tissue_08	0.02	29586	5	0.03	10560	3	0.03	0.01	0.15	653	1	0.02	5775	1	0.09	0.09
Tumor_Tissue_08	43.95	3856	3023	55.00	3349	4094	49.48	7.81	82.61	32	152	83.91	417	2175	83.26	0.92
Normal_Tissue_09	0.26	21882	58	0.31	14937	46	0.29	0.04	0.63	3486	22	8.90	1023	100	4.77	5.85
Tumor_Tissue_09	12.52	11361	1626	18.21	6915	1540	15.37	4.02	45.30	2522	2089	31.23	2215	1006	38.27	9.95
Normal_Tissue_10	0.09	28640	26	0.35	14151	50	0.22	0.18	0.87	29119	256	0.02	5623	1	0.45	0.60
Tumor_Tissue_10	78.32	1757	6346	84.76	1530	8508	81.54	4.55	94.74	857	15433	88.84	1682	13396	91.79	4.17
Normal_Tissue_11	0.21	20725	43	0.10	42019	42	0.16	0.08	1.16	6980	82	7.32	15490	1224	4.24	4.36
Tumor_Tissue_11	92.93	653	8581	93.34	1285	18022	93.14	0.29	99.76	51	21628	91.11	1850	18966	95.44	6.12
Normal_Tissue_12	0.87	26301	231	0.90	18218	165	0.89	0.02	3.38	8851	310	0.02	5569	1	1.70	2.38
Tumor_Tissue_12	96.72	645	19035	96.95	637	20249	96.84	0.16	98.21	518	28374	96.51	746	20608	97.36	1.20
Normal_Tissue_13	0.24	14132	34	0.35	31599	110	0.30	0.08	0.06	3177	2	1.35	6511	89	0.71	0.91
Tumor_Tissue_13	9.60	9220	979	9.68	11605	1244	9.64	0.06	60.47	3073	4700	71.52	1689	4241	66.00	7.81
Normal_Tissue_14	0.19	35301	67	0.00	20964	0	0.10	0.13	0.00	3943	0	0.42	4779	20	0.21	0.30
Tumor_Tissue_14	13.14	6341	959	7.88	11228	961	10.51	3.72	78.49	671	2449	84.09	543	2869	81.29	3.96
Normal_Tissue_15	0.01	33625	3	0.07	17190	12	0.04	0.04	2.07	8043	170	1.82	8103	150	1.95	0.18
Tumor_Tissue_15	81.92	739	3349	75.86	1997	6277	78.89	4.29	90.19	151	1388	96.08	26	638	93.14	4.16
Normal_Tissue_16	0.03	11468	3	0.01	15772	2	0.02	0.01	0.23	2205	5	0.86	28786	251	0.55	0.45
Tumor_Tissue_16	33.80	6144	3137	57.40	2472	3331	45.60	16.69	91.75	675	7509	73.40	715	1973	82.58	12.98
Normal_Tissue_17	0.41	35205	144	0.18	18007	33	0.30	0.16	0.00	1741	0	0.40	2715	11	0.20	0.28
Tumor_Tissue_17	60.84	2737	4253	62.20	3397	5590	61.52	0.96	34.98	2392	1287	32.61	1176	569	33.80	1.68
Normal_Tissue_18	0.31	30087	94	0.36	13995	50	0.34	0.04	0.04	2365	1	0.04	2823	1	0.04	0.00
Tumor_Tissue_18	0.05	58779	28	0.26	11409	30	0.16	0.15	75.32	801	2445	99.74	10	3839	87.53	17.27
Normal_Tissue_19	0.49	12084	60	0.18	19447	36	0.34	0.22	0.21	1917	4	0.00	2603	0	0.11	0.15
Tumor_Tissue_19	24.54	8480	2757	30.09	3796	1634	27.32	3.92	24.01	4413	1394	37.24	5829	3459	30.63	9.36
Normal_Tissue_20	0.12	23810	29	0.15	38249	57	0.14	0.02	0.00	1457	0	1.01	1276	13	0.51	0.71
Tumor_Tissue_20	30.98	5387	2418	35.87	3482	1948	33.43	3.46	71.44	1320	3302	90.83	1174	11632	81.14	13.71
Normal_Tissue_21	0.31	11065	34	0.09	17348	16	0.20	0.16	0.11	2755	3	0.02	4900	1	0.07	0.06
Tumor_Tissue_21	44.07	4082	3216	52.76	4103	4583	48.42	6.14	34.37	529	277				34.37	
Normal_Tissue_22	0.00	24845	0	0.47	16896	80	0.24	0.33	0.00	192	0	0.11	1826	2	0.06	0.08
Tumor_Tissue_22	15.62	8406	1556	12.70	10539	1533	14.16	2.06	44.67	6655	5373	37.5	8461	5077	41.09	5.07
Normal_Tissue_23	0.12	27393	34	0.25	26013	65	0.19	0.09	3.28	6465	219	10.21	4616	525	6.75	4.90
Tumor_Tissue_23	72.26	1694	4412	73.56	1825	5078	72.91	0.92	98.22	622	34244	89.03	1915	15549	93.63	6.50
Normal_Tissue_24	0.12	41963	49	0.25	32027	80	0.19	0.09	0.48	5790	28	0.59	9032	54	0.54	0.08
Tumor_Tissue_24	91.17	567	5857	91.89	1640	18576	91.53	0.51	89.55	2293	19653	92.04	1825	21105	90.80	1.76
Normal_Tissue_25	0.08	23885	18	0.36	29422	105	0.22	0.20	3.02	23054	717	0.04	23549	10	1.53	2.11
Tumor_Tissue_25	0.02	46164	8	0.07	31810	21	0.05	0.04	87.86	2839	20548	97.59	819	33199	92.73	6.88
Normal_Tissue_26	0.09	35219	31	0.02	58066	14	0.06	0.05	0.00	11943	0	0	9540	0	0.00	0.00
Tumor_Tissue_26	43.39	5073	3889	48.05	3696	3418	45.72	3.30	81.40	3435	15031	73.84	3679	10383	77.62	5.35
Normal_Tissue_27	0.22	20904	46	0.05	40975	21	0.14	0.12	4.95	8366	436	0.38	3664	14	2.67	3.23
Tumor_Tissue_27	17.12	8019	1656	14.56	9032	1539	15.84	1.81	54.17	1489	1760	66.89	1092	2206	60.53	8.99
Normal_Tissue_28	0.69	11437	80	0.46	9512	44	0.58	0.16	0.69	5044	35	7.76	5062	426	4.23	5.00
Tumor_Tissue_28	92.96	1111	14674	93.52	495	7146	93.24	0.40	96.87	320	9892	97.92	283	13291	97.40	0.74
Normal_Tissue_29	0.23	21380	50	0.47	36399	172	0.35	0.17	16.89	7226	1468	1.31	14020	186	9.10	11.02
Tumor_Tissue_29	31.97	3754	1764	38.82	4352	2761	35.40	4.84	57.33	1240	1666	69.45	1464	3328	63.39	8.57
Normal_Tissue_30	0.25	37141	94	0.59	25332	151	0.42	0.24	0.11	1880	2	0.01	6857	1	0.06	0.07
Tumor_Tissue_30	37.11	9115	5378	43.59	4239	3275	40.35	4.58	36.89	14400	8418	46.68	5854	5125	41.79	6.92
Normal_Tissue_31	2.70	6117	170	1.43	18509	268	2.07	0.90	0.14	17182	24	0.25	21313	54	0.20	0.08
Tumor_Tissue_31	56.43	4135	5355	58.90	5127	7346	57.67	1.75	81.42	4804	21051	61.86	3703	6005	71.64	13.83

Tissue Cohort #2

Tissue_ID		Concordance_Plasma	Tumoral_content	Average CH3		EYA4_%_1	unmethylated_events_1	methylated_events_1	EYA4_%_2	unmethylated_events_2	methylated_events_2	average_EYA4	STDEV_EYA4
Tumor_Tissue_33	Independent Tumors		0.6	9.20	A01	5.06	15089	804	5.53	21860	1280	5.30	0.33
Tumor_Tissue_34	Independent Tumors	CRC_Monitoring_88	0.4	34.23	B01	19.79	7445	1837	9.38	15076	1560	14.59	7.36
Tumor_Tissue_35	Independent Tumors		0.2	10.20	C01	13.21	9529	1450	7.98	13113	1137	10.60	3.70
Tumor_Tissue_36	Independent Tumors	CRC_Monitoring_86	0.3	51.77	D01	38.13	5255	3239	50.80	4921	5081	44.47	8.96
Tumor_Tissue_37	Independent Tumors	CRC_Monitoring_110	0.5	21.71	G01	4.42	3894	180	8.45	3382	312	6.44	2.85
Tumor_Tissue_38	Independent Tumors	CRC_Monitoring_118	0.6	28.47	H01	3.48	2164	78	11.82	2888	387	7.65	5.90
Tumor_Tissue_39	Independent Tumors	CRC_Monitoring_93	0.5	70.93	D05	64.57	2358	4298	53.60	2235	2582	59.09	7.76
Tumor_Tissue_40	Independent Tumors	CRC_Monitoring_90	0.5	35.92	F11	47.08	3429	3050	46.77	4616	4055	46.93	0.22
Tumor_Tissue_41	Independent Tumors	CRC_Monitoring_98		42.48	D03	35.46	2777	1526	36.38	2244	1283	35.92	0.65
Tumor_Tissue_42	Independent Tumors		0.1	36.86	F03	11.51	3974	517	19.74	5008	1232	15.63	5.82
Tumor_Tissue_43	Independent Tumors	CRC_Monitoring_107	0.2	46.62	G05	34.81	9773	5219	32.08	4625	2184	33.45	1.93
Tumor_Tissue_44	Independent Tumors	CRC_Monitoring_119		69.55	E03	51.58	1873	1995	62.63	1942	3254	57.11	7.81
Tumor_Tissue_45	Independent Tumors	CRC_Monitoring_94		14.24	H03	2.77	6202	177	4.91	7309	377	3.84	1.51
Tumor_Tissue_46	Independent Tumors		0.4	41.86	H05	33.46	3938	1980	40.19	6297	4231	36.83	4.76
Tumor_Tissue_47	Independent Tumors	CRC_Monitoring_97	0.6	63.27	B05	65.99	3648	7078	72.72	3825	10198	69.36	4.76
Tumor_Tissue_48	Independent Tumors	CRC_Monitoring_108	0.5	25.02	C05	29.11	6266	2573	37.31	7505	4466	33.21	5.80
Tumor_Tissue_49	Independent Tumors	CRC_Monitoring_102	0.5	88.99	E05	76.82	1026	3401	87.33	1243	8564	82.08	7.43
Tumor_Tissue_50	Independent Tumors	CRC_Monitoring_100	0.5	51.19	F05	49.71	2151	2126	51.44	3264	3457	50.58	1.22
Tumor_Tissue_51	Independent Tumors	CRC_Monitoring_112	0.6	92.02	B07	90.03	955	8623	93.52	907	13089	91.78	2.47
Tumor_Tissue_52	Independent Tumors	CRC_Monitoring_125	0.6	79.91	A07	81.24	1346	5829	84.15	1783	9464	82.70	2.06
Tumor_Tissue_53	Independent Tumors	CRC_Monitoring_120	0.4	25.87	C03	19.91	8727	2170	26.60	12020	4355	23.26	4.73
Tumor_Tissue_54	Independent Tumors	CRC_Monitoring_123	0.4	44.22	D07	32.58	2450	1184	43.69	3077	2387	38.14	7.86
Tumor_Tissue_55	Independent Tumors			70.15	C07	66.20	2750	5385	74.06	2809	8021	70.13	5.56
Tumor_Tissue_56	Independent Tumors		0.4	12.35	G07	1.98	4948	100	3.82	9115	362	2.90	1.30
Tumor_Tissue_57	Independent Tumors	CRC_Monitoring_104	0.6	61.03	H07	50.44	7499	7633	53.44	1457	1672	51.94	2.12
Tumor_Tissue_58	Independent Tumors	CRC_Monitoring_101	0.6	63.27	B09	23.06	5640	1690	25.98	6356	2231	24.52	2.06
Tumor_Tissue_59	Independent Tumors	CRC_Monitoring_23	0.3	55.83	C09	0.98	11811	117	1.22	17184	212	1.10	0.17
Tumor_Tissue_60	Independent Tumors	CRC_Monitoring_103		5.20	E09	0.85	5928	51	2.83	11111	324	1.84	1.40
Tumor_Tissue_61	Independent Tumors	CRC_Monitoring_96	0.7	16.29	F09	0.15	10314	16	0.20	13896	28	0.18	0.04
Tumor_Tissue_62	Independent Tumors		0.6	28.59	G09	10.74	3625	436	19.40	4080	982	15.07	6.12
Tumor_Tissue_63	Independent Tumors	CRC_Monitoring_115	0.3	68.94	G03	59.79	1480	2201	66.45	623	1234	63.12	4.71
Tumor_Tissue_64	Independent Tumors	CRC_Monitoring_126	0.3	47.46	E07	55.08	1822	2234	68.38	1664	3598	61.73	9.40
Tumor_Tissue_65	Independent Tumors	CRC_Monitoring_117	0.5	51.63	F07	43.13	2116	1605	55.24	2118	2614	49.19	8.56
Tumor_Tissue_66	Independent Tumors	CRC_Monitoring_109	0.3	21.25	A09	13.92	8679	1403	17.22	10736	2234	15.57	2.33
Tumor_Tissue_67	Independent Tumors	CRC_Monitoring_116	0.3	89.75	D09	73.67	1500	4196	83.85	1115	5789	78.76	7.20
Tumor_Tissue_68	Independent Tumors		0.4	11.64	H09	1.02	5536	57	1.66	19689	333	1.34	0.45
Tumor_Tissue_69	Independent Tumors		0.4	41.89	A11	24.40	6858	2214	32.14	6395	3029	28.27	5.47
Tumor_Tissue_70	Independent Tumors	CRC_Monitoring_1	0.4	57.32	E11	53.67	3064	3549	56.53	2907	3780	55.10	2.02
Tumor_Tissue_71	Independent Tumors	CRC_Monitoring_142	0.5	45.51	G11	32.21	4231	2010	42.02	7475	5417	37.12	6.94
Tumor_Tissue_72	Independent Tumors	CRC_Monitoring_164	0.5	31.64	A01	18.23	9097	2028	24.07	4860	1541	21.15	4.13
Tumor_Tissue_73	Independent Tumors	CRC_Monitoring_163	0.4	29.88	B01	18.51	12249	2783	14.43	10126	1707	16.47	2.88
Tumor_Tissue_74	Independent Tumors	CRC_Monitoring_153	0.1	4.11	C01	1.63	16826	279	7.79	4228	357	4.71	4.36
Tumor_Tissue_75	Independent Tumors		0.5	29.84	D01	4.25	10767	478	14.14	11261	1855	9.20	6.99
Tumor_Tissue_76	Independent Tumors	CRC_Monitoring_162	0.3	14.73	E01	12.08	15723	2161	17.90	15823	3450	14.99	4.12
Tumor_Tissue_77	Independent Tumors	CRC_Monitoring_158		40.69	F01	46.91	9642	8520	31.94	11050	5186	39.43	10.59
Tumor_Tissue_78	Independent Tumors		0.2	69.14	G01	65.83	6812	13126	60.01	7685	11531	62.92	4.12
Tumor_Tissue_79	Independent Tumors	CRC_Monitoring_159		47.52	A03	44.53	7872	6319	34.07	8488	4387	39.30	7.40
Tumor_Tissue_80	Independent Tumors		0.6	56.12	B03	43.23	8116	6181	44.36	8996	7171	43.80	0.80
Tumor_Tissue_81	Independent Tumors	CRC_Monitoring_113	0.7	47.46	A05	31.23	7319	3323	39.08	7745	4968	35.16	5.55
Tumor_Tissue_82	Independent Tumors	CRC_Monitoring_85	0.6	10.57	B11	7.85	8961	763	4.62	21434	1038	6.24	2.28
Tumor_Tissue_83	Independent Tumors	CRC_Monitoring_122	0.1	42.84	C11	21.32	4675	1267	31.57	8311	3834	26.45	7.25

Tissue_ID	GRIA4_%_1	unmethylated_events_1	methylated_events_1	GRIA4_%_2	unmethylated_events_2	methylated_events_2	average_GRIA4	STDEV_GRIA4	ITGA4_%_1	unmethylated_events_1	methylated_events_1	ITGA4_%_2	unmethylated_events_2	methylated_events_2	average_ITGA4	STDEV_ITGA4
Tumor_Tissue_33	11.63	10739	1413	12.04	20425	2796	11.84	0.29	6.50	7432	520	3.00	44740	1380	4.75	2.47
Tumor_Tissue_34	23.11	10684	3211	27.11	13181	4902	25.11	2.83	35.20	16249	8838	34.60	15246	8079	34.90	0.42
Tumor_Tissue_35	31.36	6115	2794	30.11	3444	1484	30.74	0.88	8.30	9956	907	10.90	6589	802	9.60	1.84
Tumor_Tissue_36	77.9	3082	10866	78.17	621	2224	78.04	0.19	35.80	10722	5968	34.70	8046	4284	35.25	0.78
Tumor_Tissue_37	35.84	6946	3880	37.4	7555	4514	36.62	1.10	6.00	20225	1280	6.50	16906	1176	6.25	0.35
Tumor_Tissue_38	37.05	8314	4893	43.68	3055	2369	40.37	4.69	25.30	3290	1113	21.30	2202	596	23.30	2.83
Tumor_Tissue_39	85.53	208	1229	67.35	1017	2098	76.44	12.86	47.70	2686	2445	52.90	840	942	50.30	3.68
Tumor_Tissue_40	66.63	1733	3461	68.68	3235	7094	67.66	1.45	32.30	6001	2863	22.80	5661	1669	27.55	6.72
Tumor_Tissue_41	58.53	3159	4459	56.22	5830	7487	57.38	1.63	33.30	6293	3143	30.90	2732	1219	32.10	1.70
Tumor_Tissue_42	41.23	2091	1467	37.15	1812	1071	39.19	2.88	29.40	3840	1601	25.80	2353	817	27.60	2.55
Tumor_Tissue_43	52.31	1353	1484	44.27	1761	1399	48.29	5.69	63.30	1404	2418	51.20	103	108	57.25	8.56
Tumor_Tissue_44	80.35	1654	6765	83.88	3509	18259	82.12	2.50	68.30	3339	7179	57.50	1675	2268	62.90	7.64
Tumor_Tissue_45	36.41	5148	2948	32.41	10390	4983	34.41	2.83	14.50	4848	822	10.40	1661	193	12.45	2.90
Tumor_Tissue_46	60.48	3495	5349	50.39	4346	4415	55.44	7.13	27.80	1282	493	31.70	1476	685	29.75	2.76
Tumor_Tissue_47	80.58	2140	8877	89.81	1002	8829	85.20	6.53	74.60	5628	16559	75.80	3334	10456	75.20	0.85
Tumor_Tissue_48	33.7	7097	3607	44.35	3154	2514	39.03	7.53	24.10	2340	745	17.70	7457	1602	20.90	4.53
Tumor_Tissue_49	92.4	1134	13794	92.75	1093	13980	92.58	0.25	89.00	183	1483	85.60	538	3194	87.30	2.40
Tumor_Tissue_50	76.95	2755	9196	69.54	3984	9096	73.25	5.24	38.90	1989	1264	27.60	280	107	33.25	7.99
Tumor_Tissue_51	95.54	462	9887	85.06	3289	18726	90.30	7.41	89.50	1775	15085	83.70	54	278	86.60	4.10
Tumor_Tissue_52	65.94	1434	2776	59.64	5167	7635	62.79	4.45	78.80	5299	19700	79.30	3527	13523	79.05	0.35
Tumor_Tissue_53	70.62	448	1077	76.69	242	796	73.66	4.29	23.30	1026	312	15.20	268	48	19.25	5.73
Tumor_Tissue_54	60.39	4837	7375	54.76	9663	11697	57.58	3.98	33.27	10604	5288	34.20	7166	3724	33.74	0.66
Tumor_Tissue_55	81.21	2361	10203	79.57	5450	21224	80.39	1.16	52.40	5044	5544	46.10	7636	6524	49.25	4.45
Tumor_Tissue_56	7.99	19005	1650	8.18	21493	1916	8.09	0.13	3.40	28719	1001	3.10	3842	122	3.25	0.21
Tumor_Tissue_57	78.73	4041	14962	68.41	6222	13476	73.57	7.30	29.20	8693	3580	34.00	4356	2240	31.60	3.39
Tumor_Tissue_58	79.27	2580	9863	76.86	2647	8792	78.07	1.70	59.90	4585	6844	60.40	4069	6206	60.15	0.35
Tumor_Tissue_59	89.3	1620	13520	90.35	2151	20131	89.83	0.74	93.00	1339	17782	88.00	1156	8509	90.50	3.54
Tumor_Tissue_60	9.92	7904	870	1.84	7242	136	5.88	5.71	4.40	6141	281	5.11	446	24	4.76	0.50
Tumor_Tissue_61	18.75	9571	2208	23.76	12745	3973	21.26	3.54	13.40	3126	482	10.20	8868	1012	11.80	2.26
Tumor_Tissue_62	52.65	5216	5801	46	5904	5029	49.33	4.70	16.70	6429	1289	11.80	5463	734	14.25	3.46
Tumor_Tissue_63	88.59	689	5348	79.19	5225	19889	83.89	6.65	66.80	2818	5661	64.50	2575	4685	65.65	1.63
Tumor_Tissue_64	58.04	720	996	47.54	3098	2807	52.79	7.42	22.80	5177	1529	19.80	1757	435	21.30	2.12
Tumor_Tissue_65	72.54	4010	10595	62.3	7916	13082	67.42	7.24	45.80	4158	3517	46.40	4823	4168	46.10	0.42
Tumor_Tissue_66	21.15	12337	3310	25.01	3425	1142	23.08	2.73	16.40	9959	1955	15.00	21279	3754	15.70	0.99
Tumor_Tissue_67	94.79	857	15607	94.64	1218	21494	94.72	0.11	89.20	1704	14025	87.10	1493	10089	88.15	1.48
Tumor_Tissue_68	46.16	6330	5426	51.39	6480	6851	48.78	3.70	4.40	7416	343	5.30	4250	240	4.85	0.64
Tumor_Tissue_69	74.51	1755	5130	78	1765	6259	76.26	2.47	62.40	6284	10436	59.90	3202	4792	61.15	1.77
Tumor_Tissue_70	74.06	3615	10319	72.43	4064	10679	73.25	1.15	58.30	767	1074	58.00	3212	4427	58.15	0.21
Tumor_Tissue_71	53.66	3854	4463	56.2	3836	4922	54.93	1.80	40.70	4487	3084	36.70	1468	851	38.70	2.83
Tumor_Tissue_72	62.39	16873	27994	58.03	6117	8459	60.21	3.08	2.32	1854	44	0.38	1308	5	1.35	1.37
Tumor_Tissue_73	27.84	15674	6047	23	3682	1100	25.42	3.42	24.78	762	251	17.66	2378	510	21.22	5.03
Tumor_Tissue_74	1.44	1092	16	13.17	455	69	7.31	8.29	7.29	318	25	1.40	282	4	4.35	4.16
Tumor_Tissue_75	20.86	9603	2531	22.8	4640	1370	21.83	1.37	15.74	1317	246	10.70	1661	199	13.22	3.56
Tumor_Tissue_76	3.79	17126	674	3.4	19031	670	3.60	0.28	12.06	729	100	10.21	2516	286	11.14	1.31
Tumor_Tissue_77	57.62	5816	7909	64.28	2562	4610	60.95	4.71	44.58	818	658	32.21	884	420	38.40	8.75
Tumor_Tissue_78	64.17	1231	2205	66.81	1160	2335	65.49	1.87	81.35	168	733	77.64	471	1635	79.50	2.62
Tumor_Tissue_79	55.02	3382	4137	47.25	19198	17195	51.14	5.49	35.29	2332	1272	50.07	1064	1067	42.68	10.45
Tumor_Tissue_80	63.26	9862	16980	63.27	9978	17186	63.27	0.01	55.94	8668	11005	61.01	11550	18076	58.48	3.59
Tumor_Tissue_81	57.04	235	312	56.12	1844	2358	56.58	0.65	45.50	5495	4587	41.90	857	619	43.70	2.55
Tumor_Tissue_82	15.61	7685	1421	34.26	894	466	24.94	13.19	5.20	17322	944	3.90	8587	351	4.55	0.92
Tumor_Tissue_83	59.47	5122	7514	55.98	6050	7694	57.73	2.47	36.30	14978	8527	29.40	9503	3964	32.85	4.88

Tissue_ID	MAP3K14-AS1_%_1	unmethylated_events_1	methylated_events_1	MAP3K14-AS1_%_2	unmethylated_events_2	methylated_events_2	average_MAP3K14-AS1	STDEV_MAP3K14-AS1	MSC_%_1	unmethylated_events_1	methylated_events_1	MSC_%_2	unmethylated_events_2	methylated_events_2	average_MSC	STDEV_MSC
Tumor_Tissue_33	4.93	18000	933	5.06	21940	1170	5.00	0.09	20.90	28908	7636	17.32	25602	5365	19.11	2.53
Tumor_Tissue_34	22.71	16724	4915	17.98	12972	2843	20.35	3.34	80.43	11743	48257	71.99	8466	21759	76.21	5.97
Tumor_Tissue_35	0.01	54017	4	0.11	60884	70	0.06	0.07	0.00	2072	0	0.02	4057	1	0.01	0.01
Tumor_Tissue_36	21.31	13441	3640	12.48	14083	2008	16.90	6.24	87.01	1658	11104	81.35	234	1021	84.18	4.00
Tumor_Tissue_37	12.28	17701	2478	5.18	6317	345	8.73	5.02	57.25	14780	19790	43.76	13276	10332	50.51	9.54
Tumor_Tissue_38	1.73	27404	482	0.60	4158	25	1.17	0.80	67.78	6662	14013	72.00	953	2451	69.89	2.98
Tumor_Tissue_39	60.06	4250	6390	77.57	2975	10290	68.82	12.38	99.97	12	39564	100.00	0	7999	99.99	0.02
Tumor_Tissue_40	30.07	9934	4271	36.08	9605	5421	33.08	4.25	3.69	548	21	5.09	1584	85	4.39	0.99
Tumor_Tissue_41	5.84	9423	584	9.05	19056	1897	7.45	2.27	84.39	2285	12349	74.69	3735	11022	79.54	6.86
Tumor_Tissue_42	19.82	5141	1271	29.36	9951	4136	24.59	6.75	72.09	5821	15039	82.49	148	697	77.29	7.35
Tumor_Tissue_43	16.14	9479	1825	23.05	7887	2362	19.60	4.89	87.12	369	2497	61.87	657	1066	74.50	17.85
Tumor_Tissue_44	55.05	2208	2704	57.68	6952	9477	56.37	1.86	94.83	2650	48646	83.68	3664	18788	89.26	7.88
Tumor_Tissue_45	6.41	19787	1356	8.83	11903	1153	7.62	1.71	7.66	10894	904	18.07	8552	1886	12.87	7.36
Tumor_Tissue_46	23.58	8099	2499	39.41	5617	3654	31.50	11.19	49.70	9125	9017	61.88	3961	6430	55.79	8.61
Tumor_Tissue_47	1.61	40158	658	4.10	16138	690	2.86	1.76	77.62	8462	29349	89.82	2970	26193	83.72	8.63
Tumor_Tissue_48	14.01	15664	2552	29.07	7181	2943	21.54	10.65	5.77	16832	1030	15.11	11964	2130	10.44	6.60
Tumor_Tissue_49	88.55	1988	15377	84.18	2384	12685	86.37	3.09	99.10	693	76387	94.17	1804	29158	96.64	3.49
Tumor_Tissue_50	18.21	9698	2159	23.44	13884	4251	20.83	3.70	66.96	7870	15953	89.14	2454	20144	78.05	15.68
Tumor_Tissue_51	95.77	1551	35074	90.02	2063	18610	92.90	4.07	99.77	127	55237	97.33	779	28372	98.55	1.73
Tumor_Tissue_52	85.80	2055	12417	84.18	3468	18454	84.99	1.15	93.14	2627	35667	86.95	4961	33051	90.05	4.38
Tumor_Tissue_53	9.60	11078	1177	15.75	9907	1852	12.68	4.35	0.49	7546	37	0.50	1001	5	0.50	0.01
Tumor_Tissue_54	7.79	7207	609	12.24	13636	1902	10.02	3.15	83.25	6524	32435	80.00	3578	14314	81.63	2.30
Tumor_Tissue_55	62.36	2838	4702	57.58	6247	8479	59.97	3.38	93.17	1460	19913	88.85	2783	22174	91.01	3.05
Tumor_Tissue_56	1.79	17441	317	3.61	27421	1028	2.70	1.29	43.10	12808	9700	46.49	12263	10656	44.80	2.40
Tumor_Tissue_57	56.55	3363	4377	57.53	6262	8481	57.04	0.69	92.51	3239	40033	89.53	3176	27157	91.02	2.11
Tumor_Tissue_58	56.92	6020	7953	55.82	6933	8761	56.37	0.78	98.35	1066	63428	96.17	1375	34513	97.26	1.54
Tumor_Tissue_59	0.16	58796	96	0.12	75744	91	0.14	0.03	97.48	1434	55401	97.70	1142	48467	97.59	0.16
Tumor_Tissue_60	3.36	26863	933	2.23	20374	464	2.80	0.80	11.75	3702	493	9.66	215	23	10.71	1.48
Tumor_Tissue_61	1.19	25888	313	1.36	39463	545	1.28	0.12	52.72	5691	6347	41.21	7856	5507	46.97	8.14
Tumor_Tissue_62	14.97	14592	2569	12.47	10156	1447	13.72	1.77	56.85	7796	10273	44.29	11913	9471	50.57	8.88
Tumor_Tissue_63	51.74	3466	3716	66.11	4237	8265	58.93	10.16	67.37	1568	3238	78.88	5406	20193	73.13	8.14
Tumor_Tissue_64	30.12	11389	4910	30.12	9287	4003	30.12	0.00	82.39	528	2471	60.37	7976	12149	71.38	15.57
Tumor_Tissue_65	9.17	8890	898	16.93	13742	2800	13.05	5.49	77.46	6875	23625	87.32	4326	29781	82.39	6.97
Tumor_Tissue_66	10.52	17531	2062	7.02	27219	2054	8.77	2.47	40.59	11931	8150	45.64	2274	1909	43.12	3.57
Tumor_Tissue_67	90.75	1398	13717	91.60	1176	12828	91.18	0.60	97.06	1547	51149	94.84	1931	35477	95.95	1.57
Tumor_Tissue_68	3.11	32931	1058	3.10	23696	758	3.11	0.01	0.01	44807	4	0.26	29960	78	0.14	0.18
Tumor_Tissue_69	34.66	11513	6106	43.58	9826	7591	39.12	6.31	0.45	6821	31	8.88	19044	1856	4.67	5.96
Tumor_Tissue_70	24.50	11948	3877	24.34	14579	4689	24.42	0.11	77.07	3675	12354	74.30	4417	12770	75.69	1.96
Tumor_Tissue_71	34.52	9892	5216	35.16	5795	3142	34.84	0.45	64.64	4646	8493	59.24	6792	9870	61.94	3.82
Tumor_Tissue_72	15.45	2369	433	14.76	2627	455	15.11	0.49	69.85	7605	17623	50.87	24482	25353	60.36	13.42
Tumor_Tissue_73	20.13	14596	3678	24.38	7715	2487	22.26	3.01	63.71	654	1148	64.31	14140	25475	64.01	0.42
Tumor_Tissue_74	0.42	43639	183	4.10	7491	320	2.26	2.60	3.90	592	24	0.00	2531	0	1.95	2.76
Tumor_Tissue_75	22.39	22352	6449	14.83	11121	1937	18.61	5.35	95.27	507	10221	77.39	6607	22611	86.33	12.64
Tumor_Tissue_76	9.22	18156	1844	1.82	15240	283	5.52	5.23	34.81	7181	3835	42.00	13312	9640	38.41	5.08
Tumor_Tissue_77	0.01	51414	3	0.01	38975	2	0.01	0.00	65.63	794	1516	63.66	9246	16196	64.65	1.39
Tumor_Tissue_78	63.72	4788	8409	60.30	3227	4902	62.01	2.42	73.17	9363	25536	78.43	5891	21420	75.80	3.72
Tumor_Tissue_79	30.71	5279	2340	25.02	9732	3247	27.87	4.02	85.74	6065	36460	67.51	5220	10846	76.63	12.89
Tumor_Tissue_80	26.86	5753	2113	23.33	3901	1187	25.10	2.50	96.50	2829	77964	83.39	5740	28810	89.95	9.27
Tumor_Tissue_81	12.92	22420	3327	25.87	6290	2195	19.40	9.16	76.94	5815	19406	87.99	1381	10120	82.47	7.81
Tumor_Tissue_82	0.85	35077	302	1.61	23221	380	1.23	0.54	5.28	556	31	26.48	5425	1954	15.88	14.99
Tumor_Tissue_83	23.48	14570	4472	27.01	10801	3996	25.25	2.50	72.99	7690	20781	70.87	7377	17944	71.93	1.50

Supplementary File 2G

Case_ID	Age	treatment_type	date	Response_status	Response status date	Date_CEA	CEA	Collection_Date	Extraction_kit	GE-LINE1	Sample_Type	Dataset	Days	ASM	Average CH3	Max CH3	Min CH3	Positive_sample
CRC_Monitoring_183	62							18-Nov-09	Promega	7821	Prevalence	Aging			0.10	0.31	0.00	0
CRC_Monitoring_184	60							18-Nov-09	Promega	7652	Prevalence	Aging			0.24	0.98	0.00	0
CRC_Monitoring_185	63							16-Nov-09	Promega	38733	Prevalence	Aging			0.15	0.68	0.00	0
CRC_Monitoring_186	40							17-Nov-09	Promega	16124	Prevalence	Aging			0.13	0.50	0.00	0
CRC_Monitoring_187	63							17-Nov-09	Promega	35381	Prevalence	Aging			0.46	2.23	0.00	1
CRC_Monitoring_188	62							17-Nov-09	Promega	13698	Prevalence	Aging			1.60	7.87	0.00	1
CRC_Monitoring_189	42							18-Nov-09	Promega	8156	Prevalence	Aging			0.67	3.12	0.00	1
CRC_Monitoring_190	63							18-Nov-09	Promega	13897	Prevalence	Aging			0.16	0.67	0.00	0
CRC_Monitoring_191	60							18-Nov-09	Promega	36396	Prevalence	Aging			0.49	1.68	0.00	1
CRC_Monitoring_192	41							11-Dec-09	Promega	11494	Prevalence	Aging			0.08	0.14	0.03	0
CRC_Monitoring_193	61							18-Nov-09	Promega	56746	Prevalence	Aging			0.18	0.70	0.00	0
CRC_Monitoring_194	63							19-Nov-09	Promega	14434	Prevalence	Aging			0.04	0.08	0.00	0
CRC_Monitoring_195	63							20-Nov-09	Promega	5514	Prevalence	Aging			0.19	0.72	0.00	0
CRC_Monitoring_196	65							25-Nov-09	Promega	10932	Prevalence	Aging			0.14	0.41	0.00	0
CRC_Monitoring_197	63							1-Dec-09	Promega	13638	Prevalence	Aging			0.15	0.25	0.00	0
CRC_Monitoring_198	62							27-Nov-09	Promega	17104	Prevalence	Aging			0.02	0.08	0.00	0
CRC_Monitoring_199	41							3-Dec-09	Promega	56799	Prevalence	Aging			0.01	0.03	0.00	0
CRC_Monitoring_200	43							3-Dec-09	Promega	41908	Prevalence	Aging			3.84	17.02	0.00	1
CRC_Monitoring_201	45							3-Dec-09	Promega	4982	Prevalence	Aging			0.02	0.05	0.00	0
CRC_Monitoring_202	61							4-Dec-09	Promega	5022	Prevalence	Aging			0.09	0.36	0.00	0
CRC_Monitoring_203	61							4-Dec-09	Promega	92951	Prevalence	Aging			0.19	0.78	0.00	0
CRC_Monitoring_204	61							19-Nov-09	Promega	16922	Prevalence	Aging			0.20	0.97	0.00	1
CRC_Monitoring_205	61							14-Dec-09	Promega	4573	Prevalence	Aging			0.53	2.02	0.00	1
CRC_Monitoring_206	41							14-Dec-09	Promega	30588	Prevalence	Aging			0.13	0.40	0.00	0
CRC_Monitoring_207	45							15-Dec-09	Promega	66447	Prevalence	Aging			0.03	0.09	0.00	0
CRC_Monitoring_208	62							23-Nov-09	Promega	67790	Prevalence	Aging			0.19	0.61	0.00	0
CRC_Monitoring_209	61							1-Apr-10	Promega	34482	Prevalence	Aging			0.09	0.23	0.00	0
CRC_Monitoring_210	43							17-Dec-09	Promega	21188	Prevalence	Aging			0.11	0.49	0.00	0
CRC_Monitoring_211	62							2-Apr-10	Promega	4410	Prevalence	Aging			0.16	0.60	0.00	0
CRC_Monitoring_212	65							1-Apr-10	Promega	7970	Prevalence	Aging			0.29	1.03	0.00	1
CRC_Monitoring_213	44							8-Dec-09	Promega	5048	Prevalence	Aging			0.06	0.21	0.00	0
CRC_Monitoring_214	42							10-Dec-09	Promega	7149	Prevalence	Aging			0.09	0.26	0.00	0
CRC_Monitoring_215	62							16-Dec-09	Promega	8801	Prevalence	Aging			0.01	0.04	0.00	0
CRC_Monitoring_216	45							6-Apr-10	Promega	4868	Prevalence	Aging			0.00	0.02	0.00	0
CRC_Monitoring_217	61							4-Dec-09	Promega	8264	Prevalence	Aging			0.21	0.76	0.00	0
CRC_Monitoring_218	43							9-Dec-09	Promega	9105	Prevalence	Aging			0.08	0.27	0.00	0
CRC_Monitoring_219	65							3-Dec-09	Promega	19478	Prevalence	Aging			0.11	0.36	0.00	0
CRC_Monitoring_220	40							4-Dec-09	Promega	11158	Prevalence	Aging			0.62	2.85	0.00	1
CRC_Monitoring_221	41							8-Dec-09	Promega	16463	Prevalence	Aging			0.03	0.09	0.00	0
CRC_Monitoring_222	64							8-Dec-09	Promega	9736	Prevalence	Aging			0.10	0.26	0.00	0
CRC_Monitoring_223	45							8-Dec-09	Promega	24783	Prevalence	Aging			0.05	0.11	0.00	0
CRC_Monitoring_224	64							8-Dec-09	Promega	10080	Prevalence	Aging			0.03	0.13	0.00	0
CRC_Monitoring_225	43							9-Dec-09	Promega	121208	Prevalence	Aging			0.18	0.47	0.00	0
CRC_Monitoring_226	40							10-Dec-09	Promega	8761	Prevalence	Aging			0.03	0.08	0.00	0
CRC_Monitoring_227	43							10-Dec-09	Promega	5701	Prevalence	Aging			0.04	0.12	0.00	0
CRC_Monitoring_228	62							11-Dec-09	Promega	17936	Prevalence	Aging			0.06	0.12	0.00	0
CRC_Monitoring_229	65							15-Dec-09	Promega	14304	Prevalence	Aging			0.03	0.13	0.00	0
CRC_Monitoring_230	64							16-Dec-09	Promega	3507	Prevalence	Aging			0.11	0.21	0.00	0
CRC_Monitoring_231	60							16-Dec-09	Promega	7265	Prevalence	Aging			0.02	0.07	0.00	0
CRC_Monitoring_232	64							1-Apr-10	Promega	3902	Prevalence	Aging			0.03	0.10	0.00	0
CRC_Monitoring_132	75					4-May-11	5.3	3-May-11	Promega	9992	Prevalence	Prevalence			0.23	0.95	0.00	1
CRC_Monitoring_85	76					30-Jan-12	63.5	30-Jan-12	Qiagen	37877	Prevalence	Prevalence			21.50	31.21	10.60	1
CRC_Monitoring_86	57					15-Nov-11	560	11-Nov-11	Qiagen	279826	Prevalence	Prevalence			80.32	92.80	66.95	1
CRC_Monitoring_87	45					15-Mar-12	1.1	15-Mar-12	Qiagen	18228	Prevalence	Prevalence			84.38	96.47	60.00	1
CRC_Monitoring_88	55					25-Aug-11	11.4	31-Aug-11	Qiagen	88516	Prevalence	Prevalence			2.04	7.40	0.29	1
CRC_Monitoring_89	76					8-Aug-11	66.1	9-Aug-11	Qiagen	48029	Prevalence	Prevalence			66.17	77.37	45.15	1
CRC_Monitoring_90	68					16-Jan-12	12.3	16-Jan-12	Qiagen	31253	Prevalence	Prevalence			12.12	26.71	2.27	1
CRC_Monitoring_91	54					9-Jan-12	162	9-Jan-12	Qiagen	12880	Prevalence	Prevalence			71.06	98.30	19.95	1
CRC_Monitoring_92	75					22-Aug-11	103	28-Jul-11	Qiagen	44150	Prevalence	Prevalence			8.67	13.26	3.67	1
CRC_Monitoring_93	73					5-Dec-11	101	5-Dec-11	Qiagen	16071	Prevalence	Prevalence			10.14	16.60	7.06	1
CRC_Monitoring_94	59					15-Jul-11	30.3	15-Jul-11	Qiagen	14937	Prevalence	Prevalence			23.38	35.59	1.86	1
CRC_Monitoring_95	56					9-Jun-11	444	9-Jun-11	Qiagen	168269	Prevalence	Prevalence			93.07	96.58	88.55	1
CRC_Monitoring_96	36					5-Dec-11	2057	5-Dec-11	Qiagen	74046	Prevalence	Prevalence			38.96	66.69	2.87	1
CRC_Monitoring_97	70					24-Oct-11	4.2	24-Oct-11	Qiagen	124077	Prevalence	Prevalence			73.53	93.24	34.28	1
CRC_Monitoring_98	59					28-Nov-11	300	29-Nov-11	Qiagen	20086	Prevalence	Prevalence			10.13	18.40	1.45	1
CRC_Monitoring_99	59					8-Jun-11	9.7	8-Jun-11	Qiagen	133205	Prevalence	Prevalence			65.19	84.39	23.31	1
CRC_Monitoring_100	67					3-Oct-11	869	5-Oct-11	Qiagen	278709	Prevalence	Prevalence			50.78	85.38	33.56	1
CRC_Monitoring_101	73					23-Jan-12	26.1	23-Jan-12	Qiagen	255620	Prevalence	Prevalence			85.42	95.73	67.72	1
CRC_Monitoring_102	77					28-Sep-11	969	28-Sep-11	Qiagen	108564	Prevalence	Prevalence			84.87	96.79	72.52	1
CRC_Monitoring_103	63					14-Feb-12	242	14-Feb-12	Qiagen	80164	Prevalence	Prevalence			33.86	41.78	19.89	1
CRC_Monitoring_104	49					10-Feb-12	187	10-Feb-12	Qiagen	29126	Prevalence	Prevalence			30.82	41.88	18.71	1
CRC_Monitoring_105	65					14-Mar-12	12.7	14-Mar-12	Qiagen	10283	Prevalence	Prevalence			19.10	30.94	5.85	1
CRC_Monitoring_106	66					12-Mar-12	155	12-Mar-12	Qiagen	2046	Prevalence	Prevalence			8.52	39.56	0.13	1
CRC_Monitoring_107	75					5-Sep-11	60.2	5-Sep-11	Qiagen	28040	Prevalence	Prevalence			11.82	38.60	3.68	1
CRC_Monitoring_108	58					19-Aug-11	10.8	19-Aug-11	Qiagen	12029	Prevalence	Prevalence			0.71	2.39	0.00	1
CRC_Monitoring_109	46					30-Jan-12	232	30-Jan-12	Qiagen	3700	Prevalence	Prevalence			15.56	41.57	0.08	1
CRC_Monitoring_110	37					20-Feb-12	569	20-Feb-12	Qiagen	12044	Prevalence	Prevalence			26.79	38.79	11.37	1
CRC_Monitoring_111	57					25-Aug-11	3.3	19-Sep-11	Qiagen	28588	Prevalence	Prevalence			2.83	6.48	0.93	1
CRC_Monitoring_112	54					25-Jan-12	78	26-Jan-12	Qiagen	32088	Prevalence	Prevalence			50.76	66.02	36.31	1
CRC_Monitoring_113	70					28-Nov-11	2930	29-Nov-11	Qiagen	97322	Prevalence	Prevalence			78.98	95.79	42.30	1
CRC_Monitoring_114	72					22-Aug-11	1.9	13-Sep-11	Qiagen	27680	Prevalence	Prevalence			0.50	2.35	0.00	1
CRC_Monitoring_115	42					19-Aug-11	991	12-Sep-11	Qiagen	266432	Prevalence	Prevalence			70.74	82.23	61.14	1
CRC_Monitoring_116	59					19-Aug-11	45.2	2-Sep-11	Qiagen	13432	Prevalence	Prevalence			0.02	0.06	0.00	0
CRC_Monitoring_117	41					17-Jan-12	44.8	17-Jan-12	Qiagen	17441	Prevalence	Prevalence			19.73	42.40	6.62	1
CRC_Monitoring_118	55					24-Jan-12	7.1	24-Jan-12	Qiagen	1111	Prevalence	Prevalence			2.36	10.73	0.00	1
CRC_Monitoring_119	81					10-Jun-11	168	13-Jun-11	Qiagen	350586	Prevalence	Prevalence			0.25	0.54	0.01	0
CRC_Monitoring_120	76					3-Nov-11	1600	7-Nov-11	Qiagen	51240	Prevalence	Prevalence			17.11	29.34	7.52	1
CRC_Monitoring_121	70					23-Jan-12	69.3	23-Jan-12	Qiagen	100425	Prevalence	Prevalence			76.95	95.19	29.87	1
CRC_Monitoring_122	74					12-Dec-11	282	15-Dec-11	Qiagen	83443	Prevalence	Prevalence			18.61	27.11	6.42	1
CRC_Monitoring_123	74					18-Dec-11	34.1	14-Dec-11	Qiagen	9259908	Prevalence	Prevalence			96.18	99.25	91.66	1
CRC_Monitoring_124	58					4-Aug-11	82.9	8-Aug-11	Qiagen	124285	Prevalence	Prevalence			1.40	4.04	0.09	1
CRC_Monitoring_125	71					4-Jul-11	152	4-Jul-11	Qiagen	152843	Prevalence	Prevalence			87.03	94.08	78.08	1
CRC_Monitoring_126	63					4-Nov-11	4.4	7-Nov-11	Qiagen	10695	Prevalence	Prevalence			0.22	0.74	0.00	1
CRC_Monitoring_127	73					11-Nov-11	212	11-Nov-11	Qiagen	39523	Prevalence	Prevalence			30.98	82.61	13.05	1
CRC_Monitoring_128	67					26-Sep-11	2581	26-Sep-11	Qiagen	325832	Prevalence	Prevalence			83.11	96.33	51.39	1
CRC_Monitoring_129	66					18-Jul-11	246	20-Jul-11	Qiagen	28485	Prevalence	Prevalence			81.42	89.15	45.51	1
CRC_Monitoring_1	68					9-Dec-11	100	9-Dec-11	Qiagen	52861	Prevalence	Prevalence			58.13	75.59	19.55	1
CRC_Monitoring_130	41					10-Feb-12	18.6	10-Feb-12	Qiagen	2361	Prevalence	Prevalence			0.04	0.20	0.00	0
CRC_Monitoring_131	69					30-Aug-11	79.9	1-Sep-11	Qiagen	8482	Prevalence	Prevalence			13.97	36.42	0.00	1
CRC_Monitoring_2	76					10-Nov-10	229	11-Nov-10	Promega	60603	Prevalence	Prevalence			47.19	69.83	28.72	1
CRC_Monitoring_3	47					17-Sep-14	766	15-Oct-14	Promega	26505	Prevalence	Prevalence			18.07	59.14	0.02	1
CRC_Monitoring_4	69					2-Jul-14	17.7	5-Aug-14	Promega	35085	Prevalence	Prevalence			9.30	31.59	0.02	1
CRC_Monitoring_5	49					13-Apr-15	387	8-Apr-15	Promega	35852	Prevalence	Prevalence			2.80	8.78	0.00	1
CRC_Monitoring_6	65					18-Sep-09	45.5	9-Sep-09	Promega	30699	Prevalence	Prevalence			0.07	0.31	0.00	0
CRC_Monitoring_7	56					3-May-10	3	4-May-10	Promega	30438	Prevalence	Prevalence			0.01	0.03	0.00	0
CRC_Monitoring_8	83					28-Jun-12	1738	29-Jun-12	Promega	201913	Prevalence	Prevalence			8.31	28.23	2.36	1
CRC_Monitoring_9	64					20-Jun-11	120	8-Jul-11	Promega	88960	Prevalence	Prevalence			25.02	59.68	9.33	1
CRC_Monitoring_10	68					10-Nov-14	6.4	6-Nov-14	Promega	204675	Prevalence	Prevalence			0.30	0.87	0.00	1
CRC_Monitoring_11	57					7-May-15	32.9	18-May-15	Promega	196187	Prevalence	Prevalence			11.42	26.75	1.35	1
CRC_Monitoring_12	71					23-Oct-15	9.8	23-Oct-15	Promega	84931	Prevalence	Prevalence			0.05	0.20	0.00	0
CRC_Monitoring_13	51					19-Sep-11	836	3-Oct-11	Promega	449293	Prevalence	Prevalence			80.84	96.12	45.98	1
CRC_Monitoring_14	68					25-May-11	60.5	25-May-11	Promega	19397	Prevalence	Prevalence			6.86	25.23	0.01	1
CRC_Monitoring_15	81					7-Jan-13	2.6	7-Jan-13	Promega	181457	Prevalence	Prevalence			81.69	95.29	43.39	1
CRC_Monitoring_16	73					8-Jul-15	1.1	2-Jul-15	Promega	215848	Prevalence	Prevalence			69.55	94.15	21.24	1
CRC_Monitoring_17	70					24-Jun-10	21	24-Jun-10	Promega	10659	Prevalence	Prevalence			2.11	10.33	0.00	1
CRC_Monitoring_18	55					8-Apr-15	9762	8-Apr-15	Promega	154841	Prevalence	Prevalence			66.85	83.44	37.81	1
CRC_Monitoring_19	73					23-Jun-10	8.7	25-May-10	Promega	120155	Prevalence	Prevalence			2.07	4.56	0.01	1
CRC_Monitoring_20	50					5-Dec-11	229	6-Feb-12	Promega	47478	Prevalence	Prevalence			0.97	4.74	0.00	1
CRC_Monitoring_21	74					18-Nov-13	859	18-Nov-13	Promega	131904	Prevalence	Prevalence			2.54	4.53	1.32	1
CRC_Monitoring_22	76					19-Jul-10	27.7	20-Jul-10	Promega	48021	Prevalence	Prevalence			0.07	0.21	0.00	0
CRC_Monitoring_23	70					18-Jan-11	89.3	19-Jan-11	Promega	95897	Prevalence	Prevalence			3.20	15.43	0.00	1
CRC_Monitoring_24	57					2-Sep-15	491	18-Sep-15	Promega	21321	Prevalence	Prevalence			0.04	0.08	0.00	0
CRC_Monitoring_25	61					23-Jun-10	108	23-Jun-10	Promega	1294369	Prevalence	Prevalence			10.73	19.86	2.94	1
CRC_Monitoring_26	69					28-Sep-10	1.7	19-Oct-10	Promega	157496	Prevalence	Prevalence			79.25	88.26	73.01	1
CRC_Monitoring_27	80					23-Jun-14	114	4-Aug-14	Promega	272174	Prevalence	Prevalence			25.47	43.78	1.22	1
CRC_Monitoring_28	63					20-Nov-14	7.3	20-Nov-14	Promega	409422	Prevalence	Prevalence			0.18	0.57	0.02	0
CRC_Monitoring_29	74					25-Jun-14	2.7	24-Jun-14	Promega	288828	Prevalence	Prevalence			86.00	89.70	80.37	1
CRC_Monitoring_30	69					24-Jun-14	67.4	1-Aug-14	Promega	21914	Prevalence	Prevalence			2.22	7.86	0.00	1
CRC_Monitoring_31	50					21-Jan-14	474	21-Jan-14	Promega	214074	Prevalence	Prevalence			59.98	88.95	33.04	1
CRC_Monitoring_32	70					8-Jan-15	5.5	11-Mar-15	Promega	164096	Prevalence	Prevalence			5.41	10.50	0.41	1
CRC_Monitoring_33	79					26-Jun-14	278	26-Jun-14	Promega	176953	Prevalence	Prevalence			1.01	2.21	0.04	1
CRC_Monitoring_34	82					24-Dec-10	4.3	21-Dec-10	Promega	77612	Prevalence	Prevalence			4.70	22.49	0.00	1
CRC_Monitoring_35	72					8-Jul-14	24.2	3-Sep-14	Promega	155034	Prevalence	Prevalence			12.39	28.83	1.38	1
CRC_Monitoring_36	74					17-Mar-14	4189	8-Apr-14	Promega	485303	Prevalence	Prevalence			79.59	88.15	69.70	1
CRC_Monitoring_37	70					14-Sep-10	48.5	14-Sep-10	Promega	3718001	Prevalence	Prevalence			61.31	97.22	0.32	1
CRC_Monitoring_38	72					26-Aug-14	4.8	10-Sep-14	Promega	517188	Prevalence	Prevalence			70.35	95.62	30.39	1
CRC_Monitoring_39	50					13-Aug-10	3.3	28-Jul-10	Promega	33734	Prevalence	Prevalence			9.42	39.95	0.00	1
CRC_Monitoring_40	70					14-Apr-14	17.2	14-Apr-14	Promega	10563	Prevalence	Prevalence			0.02	0.06	0.00	0
CRC_Monitoring_41	67					23-Mar-15	1.7	23-Mar-15	Promega	6879	Prevalence	Prevalence			5.50	27.36	0.00	1
CRC_Monitoring_42	72					11-Dec-12	2	11-Dec-12	Promega	25247	Prevalence	Prevalence			0.03	0.08	0.00	0
CRC_Monitoring_43	79					13-Oct-15	2	15-Oct-15	Promega	167833	Prevalence	Prevalence			0.15	0.60	0.00	0
CRC_Monitoring_44	59					5-Aug-14	8.6	5-Aug-14	Promega	103753	Prevalence	Prevalence			10.50	22.46	3.76	1
CRC_Monitoring_45	40					5-Nov-14	1267	5-Nov-14	Promega	818212	Prevalence	Prevalence			89.42	98.84	77.83	1
CRC_Monitoring_46	81					11-May-10	7.5	11-May-10	Promega	96154	Prevalence	Prevalence			0.14	0.34	0.00	0
CRC_Monitoring_47	47					10-Jun-15	31.4	10-Jun-15	Promega	28029	Prevalence	Prevalence			0.07	0.17	0.00	0
CRC_Monitoring_48	75					9-Nov-10	27	12-Oct-10	Promega	8875	Prevalence	Prevalence			0.13	0.60	0.00	0
CRC_Monitoring_49	74					20-Apr-15	12.1	8-May-15	Promega	39604	Prevalence	Prevalence			16.77	48.62	7.61	1
CRC_Monitoring_50	58					22-Jul-14	250	23-Jul-14	Promega	83437	Prevalence	Prevalence			84.34	98.00	64.04	1
CRC_Monitoring_51	68					8-May-15	71.7	8-May-15	Promega	41905	Prevalence	Prevalence			33.73	72.29	3.03	1
CRC_Monitoring_52	65					14-Jul-14	13.6	2-Sep-14	Promega	8307	Prevalence	Prevalence			0.08	0.32	0.00	0
CRC_Monitoring_53	85					30-May-14	147	30-May-14	Promega	26651	Prevalence	Prevalence			71.18	87.83	48.32	1
CRC_Monitoring_54	81					11-Sep-13	8	3-Oct-13	Promega	100139	Prevalence	Prevalence			78.86	92.89	68.27	1
CRC_Monitoring_55	61					4-Jun-13	419	5-Jun-13	Promega	1006748	Prevalence	Prevalence			98.32	99.58	97.16	1
CRC_Monitoring_56	83					27-Jan-14	194	27-Jan-14	Promega	21946	Prevalence	Prevalence			35.65	99.60	0.00	1
CRC_Monitoring_57	40					29-Oct-14	1085	30-Oct-14	Promega	31569	Prevalence	Prevalence			0.23	1.04	0.00	1
CRC_Monitoring_58	35					7-Jun-11	####	8-Jun-11	Promega	1573	Prevalence	Prevalence			0.06	0.26	0.00	0
CRC_Monitoring_59	80					22-Nov-13	235	22-Nov-13	Promega	12264	Prevalence	Prevalence			64.67	99.74	38.32	1
CRC_Monitoring_60	64					18-Mar-13	72.1	2-Apr-13	Promega	220622	Prevalence	Prevalence			0.65	1.63	0.01	1
CRC_Monitoring_61	60					25-Oct-11	1084	11-Nov-11	Promega	12394	Prevalence	Prevalence			18.65	67.60	0.00	1
CRC_Monitoring_62	56					8-Jul-10	10	22-Jul-10	Promega	7131	Prevalence	Prevalence			0.05	0.14	0.00	0
CRC_Monitoring_63	33					4-Jun-14	918	4-Jun-14	Promega	4692	Prevalence	Prevalence			1.06	4.09	0.00	1
CRC_Monitoring_64	35					25-Nov-13	54.4	23-Dec-13	Promega	32811	Prevalence	Prevalence			0.54	2.52	0.00	1
CRC_Monitoring_65	50					25-Nov-13	8.7	29-Nov-13	Promega	18510	Prevalence	Prevalence			15.66	39.38	0.00	1
CRC_Monitoring_66	43					8-Jul-13	102	8-Jul-13	Promega	32360	Prevalence	Prevalence			53.01	97.19	10.60	1
CRC_Monitoring_67	53					13-Mar-15	2	29-Jan-15	Promega	1213	Prevalence	Prevalence			0.33	1.41	0.00	1
CRC_Monitoring_68	51					15-Jul-15	39.9	15-Jul-15	Promega	46937	Prevalence	Prevalence			1.24	6.06	0.00	1
CRC_Monitoring_69	77					9-Sep-13	157	1-Oct-13	Promega	6439	Prevalence	Prevalence			0.02	0.04	0.00	0
CRC_Monitoring_70	69					20-Apr-11	8.9	20-Apr-11	Promega	1194	Prevalence	Prevalence			0.04	0.21	0.00	0
CRC_Monitoring_71	72					27-Sep-13	11.2	18-Nov-13	Promega	547401	Prevalence	Prevalence			89.16	91.38	82.66	1
CRC_Monitoring_72	39					6-Mar-12	38.3	30-Jan-12	Promega	20302	Prevalence	Prevalence			11.85	58.97	0.01	1
CRC_Monitoring_73	55					18-Jul-14	88.6	1-Aug-14	Promega	93203	Prevalence	Prevalence			44.37	91.48	13.96	1
CRC_Monitoring_74	76					2-Sep-15	43.7	2-Sep-15	Promega	107552	Prevalence	Prevalence			1.54	5.67	0.00	1
CRC_Monitoring_75	65					14-Dec-15	24.1	25-Nov-15	Promega	7137	Prevalence	Prevalence			0.93	4.49	0.00	1
CRC_Monitoring_76	62					19-Aug-15	46.4	19-Aug-15	Promega	18898	Prevalence	Prevalence			0.86	3.90	0.00	1
CRC_Monitoring_77	66					5-Jul-10	294	12-Jul-10	Promega	211771	Prevalence	Prevalence			42.85	66.21	18.49	1
CRC_Monitoring_78	58					5-Dec-14	6.3	5-Dec-14	Promega	286363	Prevalence	Prevalence			59.00	83.43	32.92	1
CRC_Monitoring_79	52					15-Jun-12	339	26-Jul-12	Promega	220328	Prevalence	Prevalence			99.33	99.95	98.43	1
CRC_Monitoring_80	51					25-Jun-13	0.8	25-Jun-13	Promega	12623	Prevalence	Prevalence			0.31	1.50	0.00	1
CRC_Monitoring_81	53					8-Jun-10	1184	15-Jun-10	Promega	25266	Prevalence	Prevalence			68.72	94.25	45.51	1
CRC_Monitoring_82	52					9-Feb-15	3.3	9-Feb-15	Promega	663475	Prevalence	Prevalence			95.16	99.13	92.97	1
CRC_Monitoring_83	50					11-Feb-13	121	28-Mar-13	Promega	58742	Prevalence	Prevalence			81.32	98.26	70.83	1
CRC_Monitoring_84	77					24-Mar-14	7.5	18-Apr-14	Promega	192325	Prevalence	Prevalence			74.94	97.55	52.77	1
CRC_Monitoring_136	59					5-Mar-13	3.3	6-Mar-13	Promega	51765	Prevalence	Prevalence			1.09	3.79	0.00	1
CRC_Monitoring_182	76					4-May-16	2.8	19-May-16	Promega	5981	Prevalence	Prevalence			3.11	9.06	0.00	1
CRC_Monitoring_181	44							12-Apr-16	Promega	13540	Prevalence	Prevalence			19.79	88.91	0.04	1
CRC_Monitoring_171	65	FOLFOX4-start	1-Jul-13			28-Jun-13	82.9	28-Jun-13	Qiagen	100149	Prevalence	Chemotherapy	0	78.41	78.41	95.38	72.22	1
CRC_Monitoring_171	65	FOLFOX4-end	1-Mar-14	SD	1-Oct-13	6-Sep-13	6.8	6-Sep-13	Qiagen	15186	longitudinal	Chemotherapy	70	0.78	0.78	2.80	0.02	1
CRC_Monitoring_171	65	Beva-FOLFIRI-start	3-Mar-14	PD	23-Jan-14	13-Dec-13	36	13-Dec-13	Qiagen	53899	longitudinal	Chemotherapy	168	57.73	57.73	82.67	45.50	1
CRC_Monitoring_171	65	Beva-FOLFIRI-end	7-May-14	Death	1-Jul-14	1-Mar-14	45	13-Feb-14	Qiagen	237271	longitudinal	Chemotherapy	230	74.05	74.05	99.22	55.42	1
CRC_Monitoring_171	65					31-Mar-14	46.4	7-May-14	Qiagen	233542	longitudinal	Chemotherapy	313	72.71	72.71	93.61	50.66	1
CRC_Monitoring_171	65					12-Jun-14	99.7											
CRC_Monitoring_172	65	FOLFOX4-start	19-Sep-13			19-Sep-13	77.8	19-Sep-13	Qiagen	162360	Prevalence	Chemotherapy	0	53.18	53.18	77.34	12.29	1
CRC_Monitoring_172	65	FOLFOX4-end	15-Jan-14	Mixted Response	20-Nov-13	9-Dec-13	29.3	20-Dec-13	Qiagen	24222	longitudinal	Chemotherapy	92	0.50	0.50	1.50	0.00	1
CRC_Monitoring_172	65	Beva-DeGramont-start	11-Feb-14	PD	1-Jan-14	12-Mar-14	28.1	25-Mar-14	Qiagen	20231	longitudinal	Chemotherapy	187	0.42	0.42	1.36	0.00	1
CRC_Monitoring_172	65	Beva-DeGramont-end	2-Sep-14	PR	20-May-14	20-May-14	20.1	20-May-14	Qiagen	21965	longitudinal	Chemotherapy	243	2.71	2.71	9.88	0.02	1
CRC_Monitoring_172	65	Beva-FOLFIRI-start	27-Oct-14	PD	12-Jan-15	14-Jul-14	23.8	18-Aug-14	Qiagen	11887	longitudinal	Chemotherapy	333	24.16	24.16	62.30	1.08	1
CRC_Monitoring_172	65	Beva-FOLFIRI-end	21-Jan-15			2-Oct-14	29	11-Nov-14	Qiagen	14493	longitudinal	Chemotherapy	418	4.20	4.20	17.60	0.00	1
CRC_Monitoring_172	65	Beva-FOLFIRI-start	2-Mar-15			12-Jan-15	20.9	22-Dec-14	Qiagen	9301	longitudinal	Chemotherapy	459	1.49	1.49	6.92	0.00	1
CRC_Monitoring_172	65	Beva-FOLFIRI-end	11-Aug-15			2-Mar-15	24.6	21-Jan-15	Qiagen	14050	longitudinal	Chemotherapy	489	1.77	1.77	8.23	0.00	1
CRC_Monitoring_172	65	Palliative	12-Aug-15			7-Apr-15	45.8	23-Mar-15	Qiagen	26548	longitudinal	Chemotherapy	550	29.51	29.51	53.99	2.07	1
CRC_Monitoring_172	65					29-Jun-15	97.5	15-Jun-15	Qiagen	29845	longitudinal	Chemotherapy	634	20.73	20.73	54.52	0.00	1
CRC_Monitoring_172	65							15-Jul-15	Qiagen	22107	longitudinal	Chemotherapy	664	42.02	42.02	97.02	8.06	1
CRC_Monitoring_173						16-Sep-13	2.3	2-Oct-13	Qiagen	37908	Prevalence	Chemotherapy	0	2.56	1.02	2.99	0.00	1
CRC_Monitoring_174						24-Oct-13	49.8	10-Feb-14	Qiagen	9661	Prevalence	Chemotherapy	0		0.04	0.14	0.00	0
CRC_Monitoring_175	67					29-Apr-14	79	29-Apr-14	Qiagen	341927	Prevalence	Chemotherapy	0	52.28	52.28	87.17	0.78	1
CRC_Monitoring_176	45	FOLFIRI-start	14-May-14			26-May-14	518	12-May-14	Qiagen	7014008	Prevalence	Chemotherapy	0	95.50	95.50	97.75	93.45	1
CRC_Monitoring_176	45	FOLFIRI-end	17-Jul-14	Mixed Response	25-Jun-14			9-Jun-14	Qiagen	84081	longitudinal	Chemotherapy	28	44.82	44.82	80.92	2.00	1
CRC_Monitoring_176	45			PD	9-Jul-14	26-Jun-14	308	25-Jun-14	Qiagen	58684	longitudinal	Chemotherapy	44	44.10	44.10	66.24	21.70	1
CRC_Monitoring_176	45			Death	1-Aug-14			15-Jul-14	Qiagen	397544	longitudinal	Chemotherapy	58	77.41	77.41	93.62	66.84	1
CRC_Monitoring_177	77	Beva-FOLFIRI-start	13-May-14			13-May-14	455	13-May-14	Qiagen	29728	Prevalence	Chemotherapy	0	37.84	30.30	66.44	0.12	1
CRC_Monitoring_177	77	Beva-FOLFIRI-end	15-Jul-14	SD dimensional / PD clinic	6-Aug-14			27-May-14	Qiagen	30848	longitudinal	Chemotherapy	14	20.92	16.12	62.70	0.01	1
CRC_Monitoring_177	77	Palliative	16-Jul-14			10-Jun-14	362.4	10-Jun-14	Qiagen	27968	longitudinal	Chemotherapy	28	8.04	6.50	13.69	0.11	1
CRC_Monitoring_177	77							25-Jun-14	Qiagen	42135	longitudinal	Chemotherapy	43	8.86	26.16	95.35	0.03	1
CRC_Monitoring_177	77					15-Jul-14	1070	15-Jul-14	Qiagen	36197	longitudinal	Chemotherapy	63	34.44	33.62	57.77	8.73	1
CRC_Monitoring_177	77					6-Aug-14	3278	19-Aug-14	Qiagen	7881452	longitudinal	Chemotherapy	98	29.75	36.38	62.89	2.22	1
CRC_Monitoring_178	62	Beva-FOLFOX-start	2-Jul-13			2-Jul-13	527	2-Jul-13	Qiagen	95599	Prevalence	Chemotherapy	0	43.64	43.64	64.39	15.39	1
CRC_Monitoring_178	62	Beva-FOLFOX-end	18-Dec-13	PR	1-Sep-13	10-Sep-13	14.9	10-Sep-13	Qiagen	9759	longitudinal	Chemotherapy	70	0.03	0.03	0.15	0.00	0
CRC_Monitoring_178	62	FOLFIRI-start	4-Feb-14	PD	1-Jan-14	9-Dec-13	83.5	14-Jan-14	Qiagen	47443	longitudinal	Chemotherapy	196	24.52	24.52	39.78	12.46	1
CRC_Monitoring_178	62	FOLFIRI-end	2-Apr-14			3-Feb-14	791	14-Apr-14	Qiagen	38313	longitudinal	Chemotherapy	286	64.44	64.44	78.94	49.17	1
CRC_Monitoring_178	62					18-Mar-14	878											
CRC_Monitoring_178	62					31-Mar-14	1197											
CRC_Monitoring_179	54							3-Jul-13	Qiagen	21720	Prevalence	Chemotherapy	0	1.58	9.99	48.35	0.00	1
CRC_Monitoring_180	68	Beva-FOLFOX-start	23-Jul-13			15-Jul-13	28.9	15-Jul-13	Qiagen	69420	Prevalence	Chemotherapy	0	59.93	59.93	76.80	41.67	1
CRC_Monitoring_180	68	Beva-FOLFOX-end	5-Mar-14	PR	1-May-14	9-Oct-13	7.3	21-Oct-13	Qiagen	23076	longitudinal	Chemotherapy	98	1.34	1.34	3.01	0.00	1
CRC_Monitoring_180	68	Beva-DeGramont-start	1-Apr-14	PD	1-Sep-14	30-Dec-13	4.5	3-Feb-14	Qiagen	52987	longitudinal	Chemotherapy	203	0.50	0.50	2.34	0.00	1
CRC_Monitoring_180	68	Beva-DeGramont-end	27-May-14			15-Feb-14	4.7	12-May-14	Qiagen	26961	longitudinal	Chemotherapy	301	11.11	11.11	41.79	0.03	1
CRC_Monitoring_180	68	FOLFIRI-start	16-Sep-14			28-May-14	4.9	3-Jul-14	Qiagen	38802	longitudinal	Chemotherapy	353	39.15	39.15	75.20	13.75	1
CRC_Monitoring_180	68	FOLFIRI-end	13-May-15			29-Oct-14	5.1	15-Sep-14	Qiagen	13961	longitudinal	Chemotherapy	427	10.63	10.63	30.30	0.02	1
CRC_Monitoring_140	68	Beva-FOLFOX-start	3-Jun-16	SD	6-Sep-16	1-Jun-16	75.8	1-Jun-16	Promega	101355	Prevalence	Chemotherapy	0	81.80	65.46	96.53	0.09	1
CRC_Monitoring_140	68							21-Jun-16	Promega	44388	longitudinal	Chemotherapy	20	51.87	41.51	67.95	0.10	1
CRC_Monitoring_140	68							18-Jul-16	Promega	45691	longitudinal	Chemotherapy	47	1.66	1.78	2.32	1.09	1
CRC_Monitoring_140	68					21-Jun-16	149	1-Aug-16	Promega	24586	longitudinal	Chemotherapy	61	0.93	12.69	59.73	0.01	1
CRC_Monitoring_140	68					25-Oct-16	56	17-Aug-16	Promega	44081	longitudinal	Chemotherapy	77	0.56	0.88	2.20	0.00	1
CRC_Monitoring_140	68							30-Aug-16	Promega	42876	longitudinal	Chemotherapy	90	0.12	0.39	1.43	0.00	1
CRC_Monitoring_141	62	Beva-FOLFOX-start	13-May-16	PR	19-Jul-16	11-May-16	56.3	19-May-16	Promega	20210	Prevalence	Chemotherapy	0	78.24	78.24	97.78	52.36	1
CRC_Monitoring_141	62			PR	1-Sep-16			4-Jul-16	Promega	44711	longitudinal	Chemotherapy	76	0.02	0.02	0.05	0.00	0
CRC_Monitoring_141	62							19-Jul-16	Promega	47809	longitudinal	Chemotherapy	91	0.60	0.60	2.39	0.04	1
CRC_Monitoring_141	62							2-Aug-16	Promega	33231	longitudinal	Chemotherapy	105	0.16	0.16	0.71	0.00	1
CRC_Monitoring_141	62							16-Aug-16	Promega	15860	longitudinal	Chemotherapy	119	0.05	0.05	0.13	0.00	0
CRC_Monitoring_141	62							29-Aug-16	Promega	27284	longitudinal	Chemotherapy	132	0.71	0.71	3.14	0.00	1
CRC_Monitoring_133	46	Panitumumab - start	11-Jul-13	PR	10-Jan-14	11-Jul-13	3321	11-Jul-13	Promega	133064	Prevalence	EGFRi	0	38.46	30.85	83.65	0.41	1
CRC_Monitoring_133	46	Panitumumab - end	11-Apr-14	PD	11-Apr-14			26-Jul-13	Qiagen	23597	longitudinal	EGFRi	15	2.27	1.94	9.03	0.00	1
CRC_Monitoring_133	46							20-Aug-13	Qiagen	22726	longitudinal	EGFRi	40	1.46	1.17	5.75	0.00	1
CRC_Monitoring_133	46							3-Sep-13	Qiagen	24621	longitudinal	EGFRi	54	0.05	0.04	0.19	0.00	0
CRC_Monitoring_133	46							3-Oct-13	Promega	12837	longitudinal	EGFRi	84	0.36	0.32	1.33	0.00	1
CRC_Monitoring_133	46					30-Dec-13	71	16-Jan-14	Qiagen	24798	longitudinal	EGFRi	189	28.73	22.99	76.79	0.00	1
CRC_Monitoring_133	46							3-Apr-14	Qiagen	2532635	longitudinal	EGFRi	266	50.31	40.46	90.00	0.06	1
CRC_Monitoring_134	53	Panitumumab - start	5-Nov-13	PR	12-Apr-12	16-Feb-12	8828	16-Feb-12	Promega	2400999	Prevalence	EGFRi	0	87.13	87.13	97.41	69.75	1
CRC_Monitoring_134	53	Panitumumab - end	20-Mar-14	PD	14-Sep-12			15-Mar-12	Qiagen	176978	longitudinal	EGFRi	28	0.88	0.88	3.76	0.00	1
CRC_Monitoring_134	53	Irinotecan - start	1-Sep-14			29-Mar-12	360	12-Apr-12	Promega	177880	longitudinal	EGFRi	56	0.65	0.65	2.24	0.00	1
CRC_Monitoring_134	53							21-Jun-12	Qiagen	334573	longitudinal	EGFRi	126	0.80	0.80	1.87	0.00	1
CRC_Monitoring_134	53							5-Jul-12	Promega	24850	longitudinal	EGFRi	140	6.47	6.47	14.66	0.25	1
CRC_Monitoring_134	53							2-Aug-12	Promega	200639	longitudinal	EGFRi	168	57.07	57.07	89.54	11.04	1
CRC_Monitoring_134	53							16-Aug-12	Qiagen	196545	longitudinal	EGFRi	182	54.54	54.54	75.11	35.47	1
CRC_Monitoring_134	53							31-Aug-12	Qiagen	414699	longitudinal	EGFRi	197	55.77	55.77	83.57	43.14	1
CRC_Monitoring_134	53							14-Sep-12	Promega	324263	longitudinal	EGFRi	211	52.78	52.78	83.12	26.42	1
CRC_Monitoring_135	70	Panitumumab - start	2-Aug-11	SD	17-Aug-11	29-Jul-11	39.3	29-Jul-11	Qiagen	11590	Prevalence	EGFRi	0	48.81	39.05	59.04	0.00	1
CRC_Monitoring_135	70			SD	28-Sep-11			17-Aug-11	Qiagen	7866	longitudinal	EGFRi	19	2.28	2.14	8.90	0.00	1
CRC_Monitoring_135	70			PD	6-Dec-11			28-Sep-11	Qiagen	22098	longitudinal	EGFRi	61	0.79	0.68	3.03	0.00	1
CRC_Monitoring_135	70							11-Oct-11	Qiagen	12698	longitudinal	EGFRi	74	1.76	1.47	7.02	0.00	1
CRC_Monitoring_135	70							6-Dec-11	Qiagen	14734	longitudinal	EGFRi	130	25.77	25.77	43.17	0.00	1
CRC_Monitoring_135	71							6-Feb-12	Qiagen	13984	longitudinal	EGFRi	192	73.11	72.29	100.00	54.53	1
CRC_Monitoring_137	46					23-Jul-10	1.3	23-Jul-10	Qiagen	28860	Prevalence	EGFRi			0.02	0.06	0.00	0
CRC_Monitoring_138	83	Panitumumab - start	2-May-13			16-May-13	60.4	30-Apr-13	Promega	80205	Prevalence	EGFRi	0	1.96	1.26	2.79	0.00	1
CRC_Monitoring_138	83	Panitumumab - end	28-Oct-13	PD				19-Jul-13	Qiagen	51181	longitudinal	EGFRi	80	6.50	4.04	9.78	0.00	1
CRC_Monitoring_138	83	Irinotecan - start	4-Jan-14			18-Oct-13	29.7	6-Nov-13	Qiagen	1012589	longitudinal	EGFRi	190	9.84	6.47	18.33	0.00	1
CRC_Monitoring_138	83							14-Jan-14	Promega	489943	longitudinal	EGFRi	259	39.62	37.47	50.24	20.20	1
CRC_Monitoring_138	83							29-Jan-14	Promega	449804	longitudinal	EGFRi	274	11.15	14.57	25.72	7.80	1
CRC_Monitoring_139	75	Panitumumab - start	23-May-13			22-May-13	2.6	22-May-13	Qiagen	24183	Prevalence	EGFRi	0	2.41	1.93	6.97	0.00	1
CRC_Monitoring_139	75	Panitumumab - end	24-Oct-13	PD	4-Oct-13			19-Jun-13	Qiagen	28611	longitudinal	EGFRi	28	14.20	11.36	40.94	0.00	1
CRC_Monitoring_139	75	Irinotecan - start	24-Oct-13	PD	5-Feb-14			17-Jul-13	Qiagen	23953	longitudinal	EGFRi	56	17.35	13.88	59.54	0.01	1
CRC_Monitoring_139	75							21-Aug-13	Qiagen	25726	longitudinal	EGFRi	91	37.73	30.39	56.32	0.04	1
CRC_Monitoring_139	75					3-Jul-13	11.8	18-Sep-13	Qiagen	45577	longitudinal	EGFRi	119	47.44	38.91	94.86	0.10	1
CRC_Monitoring_139	75							24-Oct-13	Qiagen	85345	longitudinal	EGFRi	155	64.63	53.28	96.26	0.23	1
CRC_Monitoring_139	75							29-Nov-13	Qiagen	31490	longitudinal	EGFRi	191	67.07	53.82	84.10	0.11	1
CRC_Monitoring_139	75							3-Jan-14	Qiagen	49563	longitudinal	EGFRi	226	10.94	8.75	31.31	0.01	1
CRC_Monitoring_142	60			SD	8-Feb-13	28-Dec-12	164	28-Dec-12	Qiagen	44484	Prevalence	TEMECT	0	34.54	34.54	84.63	8.02	1
CRC_Monitoring_142	60			PD	22-Mar-13	9-Jan-13	107.3	9-Jan-13	Qiagen	43962	longitudinal	TEMECT	12	19.75	19.75	67.62	6.09	1
CRC_Monitoring_142	60					25-Jan-13	197.4	25-Jan-13	Qiagen	41918	longitudinal	TEMECT	28	50.25	50.25	61.71	42.29	1
CRC_Monitoring_142	60					20-Feb-13	150.4	20-Feb-13	Qiagen	32582	longitudinal	TEMECT	54	47.55	47.55	73.31	33.27	1
CRC_Monitoring_142	60					1-Mar-13	209.4	1-Mar-13	Qiagen	2581	longitudinal	TEMECT	63	37.98	37.98	51.27	23.01	1
CRC_Monitoring_143	61			SD	8-Mar-13	24-Jan-13	44.5	25-Jan-13	Qiagen	48357	Prevalence	TEMECT	0	51.44	51.44	78.32	1.51	1
CRC_Monitoring_143	61			SD	19-Apr-13	14-Feb-13	30.3	14-Feb-13	Qiagen	10232	longitudinal	TEMECT	20	3.78	3.78	11.23	0.02	1
CRC_Monitoring_143	61					20-Feb-13	32.5	20-Feb-13	Qiagen	18877	longitudinal	TEMECT	26	0.15	0.15	0.40	0.00	0
CRC_Monitoring_143	61					8-Mar-13	48.5	4-Mar-13	Qiagen	35012	longitudinal	TEMECT	38	5.79	5.79	12.10	0.00	1
CRC_Monitoring_143	61					27-Mar-13	92.1	27-Mar-13	Qiagen	64785	longitudinal	TEMECT	61	54.21	54.21	98.00	3.39	1
CRC_Monitoring_143	61					19-Apr-13	115.6	23-Apr-13	Qiagen	98241	longitudinal	TEMECT	88	68.00	68.00	98.34	8.28	1
CRC_Monitoring_144	54			SD	10-Oct-13	23-Aug-13	13.3	23-Aug-13	Qiagen	17574	Prevalence	TEMECT	0	2.27	2.74	4.64	1.03	1
CRC_Monitoring_144	54			SD	20-Nov-13	22-Oct-13	29.3	23-Oct-13	Qiagen	15894	longitudinal	TEMECT	61	13.64	14.79	22.27	4.47	1
CRC_Monitoring_144	54			PD	3-Jan-14	17-Dec-13	22	18-Dec-13	Qiagen	100167	longitudinal	TEMECT	117	62.69	64.78	86.24	36.66	1
CRC_Monitoring_144	54					13-Jan-14	25.7	27-Jan-14	Qiagen	1037212	longitudinal	TEMECT	157	72.68	74.42	94.59	44.45	1
CRC_Monitoring_145	62			PD	3-Feb-14	19-Dec-13	60	19-Dec-13	Qiagen	11774	Prevalence	TEMECT	0	1.97	0.48	1.97	0.00	1
CRC_Monitoring_145	62					22-Jan-14	117.9	22-Jan-14	Qiagen	111113	longitudinal	TEMECT	34	1.23	2.52	10.50	0.01	1
CRC_Monitoring_146	72			SD	21-Aug-13	5-Jul-13	147.6	5-Jul-13	Qiagen	19981	Prevalence	TEMECT	0	15.57	12.52	29.43	0.30	1
CRC_Monitoring_146	72			PD	3-Oct-13	8-Aug-13	238.1	8-Aug-13	Qiagen	16859	longitudinal	TEMECT	34	40.51	35.54	48.98	15.65	1
CRC_Monitoring_146	72					5-Sep-13	309.1	5-Sep-13	Qiagen	13415	longitudinal	TEMECT	62	52.13	41.85	94.43	0.76	1
CRC_Monitoring_146	72					5-Sep-13	334.5	12-Sep-13	Qiagen	41701	longitudinal	TEMECT	69	83.95	75.96	95.21	43.98	1
CRC_Monitoring_146	72					9-Oct-13	592.3	10-Oct-13	Qiagen	41418	longitudinal	TEMECT	97	61.68	59.51	76.92	45.76	1
CRC_Monitoring_147	77			SD	15-Oct-13	3-Sep-13	112.9	3-Sep-13	Qiagen	34425	Prevalence	TEMECT	0	29.32	29.32	73.59	1.51	1
CRC_Monitoring_147	77			PD	29-Nov-13	2-Oct-13	52.3	2-Oct-13	Qiagen	35262	longitudinal	TEMECT	29	2.16	2.16	9.16	0.00	1
CRC_Monitoring_147	77					30-Oct-13	16.6	30-Oct-13	Qiagen	24736	longitudinal	TEMECT	57	2.23	2.23	6.78	0.10	1
CRC_Monitoring_148	63			PD	11-Mar-13	23-Jan-13	2389	21-Jan-13	Qiagen	70062	Prevalence	TEMECT	0	77.75	77.75	96.31	64.43	1
CRC_Monitoring_148	63					11-Feb-13	3440	11-Feb-13	Qiagen	140043	longitudinal	TEMECT	21	88.22	88.22	96.05	79.93	1
CRC_Monitoring_149	63			PD	6-Mar-13	14-Jan-13	1866	14-Jan-13	Qiagen	35597	Prevalence	TEMECT	0	12.78	12.78	25.45	3.94	1
CRC_Monitoring_149	63					30-Jan-13	2148	11-Feb-13	Qiagen	26031	longitudinal	TEMECT	28	27.34	27.34	59.01	0.68	1
CRC_Monitoring_149	63					8-Mar-13	2446	8-Mar-13	Qiagen	56424	longitudinal	TEMECT	53	49.34	49.34	79.48	17.89	1
CRC_Monitoring_150	62					3-May-13	132	4-Apr-13	Qiagen	21605	Prevalence	TEMECT	0	0.78	0.78	3.76	0.00	1
CRC_Monitoring_151	45			PD	21-Jun-13	6-May-13	11	6-May-13	Qiagen	19490	Prevalence	TEMECT	0	72.66	72.66	99.22	56.50	1
CRC_Monitoring_151	45					7-Jun-13	21.6	7-Jun-13	Qiagen	60633	longitudinal	TEMECT	32	84.48	84.48	89.41	81.91	1
CRC_Monitoring_151	45					3-Jul-13	52.7	5-Jul-13	Qiagen	51833	longitudinal	TEMECT	60	88.90	88.90	99.04	81.32	1
CRC_Monitoring_152	47			SD	8-May-13	11-Mar-13	19.2	14-Mar-13	Qiagen	23568	Prevalence	TEMECT	0	37.39	37.39	69.56	11.72	1
CRC_Monitoring_152	47			PD	18-May-13	28-Mar-13	23.5	26-Mar-13	Qiagen	7785	longitudinal	TEMECT	12	13.29	13.29	40.36	0.57	1
CRC_Monitoring_152	47					24-Apr-13	40	24-Apr-13	Qiagen	13265	longitudinal	TEMECT	41	14.83	14.83	40.23	2.75	1
CRC_Monitoring_152	47					8-May-13	41.7	22-May-13	Qiagen	5556	longitudinal	TEMECT	69	40.24	40.24	91.27	2.04	1
CRC_Monitoring_152	47					20-Jun-13	119.9	20-Jun-13	Qiagen	17013	longitudinal	TEMECT	98	58.79	58.79	94.21	16.54	1
CRC_Monitoring_153	41			PR	3-May-13	21-Mar-13	84.1	21-Mar-13	Qiagen	14536	Prevalence	TEMECT	0	80.58	80.58	98.87	59.55	1
CRC_Monitoring_153	41			PR	4-Jun-13	3-May-13	176.7	3-May-13	Qiagen	25979	longitudinal	TEMECT	43	71.24	71.24	90.37	54.27	1
CRC_Monitoring_153	41			SD	27-Jun-13	28-May-13	246.9	4-Jun-13	Qiagen	36216	longitudinal	TEMECT	75	57.10	57.10	66.55	43.54	1
CRC_Monitoring_153	41			PD	4-Sep-13	27-Jun-13	449	27-Jun-13	Qiagen	72514	longitudinal	TEMECT	98	88.89	88.89	99.67	74.89	1
CRC_Monitoring_153	41					5-Sep-13	1073	4-Sep-13	Qiagen	197007	longitudinal	TEMECT	167	87.02	87.02	99.40	77.84	1
CRC_Monitoring_154	57			PD	15-Mar-13	25-Jan-13	406.6	25-Jan-13	Qiagen	40465	Prevalence	TEMECT	0	16.41	16.41	28.96	4.76	1
CRC_Monitoring_154	57					25-Feb-13	666.8	25-Feb-13	Qiagen	53501	longitudinal	TEMECT	31	42.31	42.31	79.27	16.08	1
CRC_Monitoring_154	57					26-Mar-13	780.3	26-Mar-13	Qiagen	30809	longitudinal	TEMECT	60	57.75	57.75	95.78	27.19	1
CRC_Monitoring_155	55					11-Apr-13	634.7	3-Apr-13	Qiagen	104241	Prevalence	TEMECT	0	35.56	35.56	58.54	18.23	1
CRC_Monitoring_155	55							11-Apr-13	Qiagen	1081552	longitudinal	TEMECT	8	63.21	63.21	94.02	42.09	1
CRC_Monitoring_155	55					9-May-13	1629	9-May-13	Qiagen	245753	longitudinal	TEMECT	36	65.26	65.26	92.15	50.50	1
CRC_Monitoring_156	55			PD	12-Jun-13	10-Apr-13	88.4	10-Apr-13	Qiagen	6089	Prevalence	TEMECT	0	0.77	0.17	0.77	0.00	1
CRC_Monitoring_156	55					30-Apr-13	80.6	30-Apr-13	Qiagen	17227	longitudinal	TEMECT	20	1.76	9.78	27.30	1.76	1
CRC_Monitoring_156	55					28-May-13	104.7	28-May-13	Qiagen	19510	longitudinal	TEMECT	48	16.71	24.09	64.17	1.38	1
CRC_Monitoring_156	55					2-Jul-13	111.5	2-Jul-13	Qiagen	18086	longitudinal	TEMECT	83	38.66	45.40	68.01	34.43	1
CRC_Monitoring_157	64					4-Apr-13	5	4-Apr-13	Qiagen	18012	Prevalence	TEMECT	0	11.83	2.43	11.83	0.00	1

CRC_Monitoring_158	62			SD	8-Apr-14	27-Feb-14	6.8	28-Feb-14	Qiagen	16364	Prevalence	TEMECT	0	14.62	6.04	28.48	0.00	1						28.48	0.76	0.00	0.01	0.93																	57.80		25.38	638	217	31.58	4129	1906	28.48	4.38	1.5	12371	190	0.02	20752	4	0.76	1.05	0	12160	0	0	2005	0	0.00	0.00	0	24772	0	0.01	22542	3	0.01	0.01	0.19	527	1	1.67	825	14	0.93	1.05
CRC_Monitoring_158	62			SD	20-May-14	21-Mar-14	3.11	27-Mar-14	Qiagen	6589	longitudinal	TEMECT	27	0.03	1.33	6.50	0.00	1						0.01	0.06	6.50	0.00	0.10																			0	227	0	0.02	5245	1	0.01	0.01	0.04	43313	17	0.07	13168	9	0.06	0.02	0	246	0	12.99	375	56	6.50	9.19	0	3476	0	0	883	0	0.00	0.00	0.2	502	1	0	342	0	0.10	0.14
CRC_Monitoring_158	62					7-May-14	2.85	7-May-14	Qiagen	9424	longitudinal	TEMECT	68	5.18	3.67	10.29	0.06	1						10.29	0.06	0.10	3.22	4.69																			16.94	1162	237	3.63	716	27	10.29	9.41	0.07	65802	43	0.05	15695	8	0.06	0.01	0.18	550	1	0.01	7436	1	0.10	0.12	0	5795	0	6.44	218	15	3.22	4.55	1.72	171	3	7.66	2181	181	4.69	4.20
CRC_Monitoring_158	62					24-May-14	11.2	21-May-14	Qiagen	18090	longitudinal	TEMECT	82	0.79	1.44	5.09	0.02	1						1.50	0.08	0.54	0.02	5.09																			3	323	10	0	4711	0	1.50	2.12	0.09	37495	33	0.06	30493	19	0.08	0.02	1.07	1295	14	0	4361	0	0.54	0.76	0.03	6292	2	0	21120	0	0.02	0.02	10.17	433	49	0	1038	0	5.09	7.19
CRC_Monitoring_158	62					21-Jun-14	23	25-Jun-14	Qiagen	11687	longitudinal	TEMECT	117	0.03	2.09	9.95	0.00	1						0.03	0.03	0.44	0.00	9.95																			0.06	4721	3	0	566	0	0.03	0.04	0.01	13987	2	0.04	31502	13	0.03	0.02	0	675	0	0.88	112	1	0.44	0.62	0	670	0	0	3927	0	0.00	0.00	0	267	0	19.9	334	83	9.95	14.07
CRC_Monitoring_159	55			PD	3-Feb-14	16-Dec-13	262.8	17-Dec-13	Qiagen	32537	Prevalence	TEMECT	0	17.83	17.83	48.01	1.88	1						48.01	10.41	1.88	7.18	21.66																	8.80		39.09	8769	5628	56.92	1525	2015	48.01	12.61	4.4	10496	481	16.42	4453	875	10.41	8.50	3.75	5562	217	0.01	7124	1	1.88	2.64	12.01	4295	586	2.35	23650	570	7.18	6.83	29.57	162	68	13.74	3686	587	21.66	11.19
CRC_Monitoring_159	55					22-Jan-14	373	22-Jan-14	Qiagen	33975	longitudinal	TEMECT	36	36.21	36.21	79.50	18.18	1						32.37	18.18	79.50	23.14	27.88																			25.51	21562	7383	39.23	2666	1721	32.37	9.70	25.33	31473	10674	11.02	23252	2879	18.18	10.12	78.66	4009	14776	80.33	3333	13615	79.50	1.18	21.89	13786	3864	24.39	50512	16297	23.14	1.77	24.92	943	313	30.84	2119	945	27.88	4.19
CRC_Monitoring_159	55					19-Feb-14	523.4	19-Feb-14	Qiagen	19696	longitudinal	TEMECT	64	45.17	45.17	77.29	27.56	1						27.56	34.40	77.29	45.01	41.58																			33.35	25622	12820	21.76	15657	4355	27.56	8.20	44.96	836	683	23.84	11290	3534	34.40	14.93	64.07	4920	8772	90.5	427	4066	77.29	18.69	40.41	5201	3527	49.6	36815	36230	45.01	6.50	42.96	478	360	40.19	1765	1186	41.58	1.96
CRC_Monitoring_160	74			SD	4-Apr-14	18-Feb-14	280	18-Feb-14	Qiagen	23854	Prevalence	TEMECT	0	47.45	47.45	98.39	9.83	1					NA	47.06	9.83	98.39	34.51						NA												0.00		45.64	1547	1299	48.48	2713	2553	47.06	2.01	10.53	1895	223	9.13	20561	2067	9.83	0.99	96.8	9	272	99.98	1	4724	98.39	2.25	38.69	5371	3390	30.32	10974	4776	34.51	5.92								
CRC_Monitoring_160	74					20-Mar-14	370.9	20-Mar-14	Qiagen	16391	longitudinal	TEMECT	30	46.71	47.06	86.38	26.53	1						44.93	26.53	86.38	28.99	48.49																			44.93	2166	1767				44.93		27.5	8863	3361	25.56	30781	10567	26.53	1.37	82.39	1294	6053	90.37	3410	31985	86.38	5.64	25.05	21728	7262	32.92	2576	1264	28.99	5.56	45.78	315	266	51.2	304	319	48.49	3.83
CRC_Monitoring_160	74					18-Apr-14	658.4	17-Apr-14	Qiagen	43793	longitudinal	TEMECT	58	55.61	49.58	92.96	25.46	1						47.67	34.09	92.96	47.73	25.46																			47.67	1225	1116				47.67	2.60	27.92	24660	9550	40.26	17486	11785	34.09	8.73	87.24	3673	25105	98.68	637	47456	92.96	8.09	45.95	2564	2180	49.5	23593	23128	47.73	2.51	19.66	2468	604	31.25	462	210	25.46	8.20
CRC_Monitoring_161	68			SD	23-Apr-14	5-Mar-14	22	4-Mar-14	Qiagen	28577	Prevalence	TEMECT	0	4.53	2.84	5.87	0.29	1						0.35	5.87	0.29	3.66	4.05																	0.60		0.69	16477	115	0	13250	0	0.35	0.49	6.1	11686	757	5.64	24618	1471	5.87	0.33	0.57	4575	26	0	3097	0	0.29	0.40	5.61	5436	323	1.71	19614	342	3.66	2.76	8.1	193	17	0	980	0	4.05	5.73
CRC_Monitoring_161	68			PD	30-May-14	9-Apr-14	37.4	9-Apr-14	Qiagen	6535	longitudinal	TEMECT	36	16.11	9.66	45.69	0.00	1						0.00	2.19	0.00	45.69	0.44																			0	6986	0	0	315	0	0.00	0.00	0.07	8858	6	4.3	4204	189	2.19	2.99	0	675	0	0	1751	0	0.00	0.00	46.31	2722	2348	45.07	924	758	45.69	0.88	0.58	171	1	0.29	346	1	0.44	0.21
CRC_Monitoring_161	68					7-May-14	47.6	7-May-14	Qiagen	10376	longitudinal	TEMECT	64	13.41	8.08	25.38	0.00	1						0.16	14.86	0.02	25.38	0.00																			0.16	3810	6				0.16		19.7	7265	1782	10.01	27886	3101	14.86	6.85	0.03	3385	1	0.01	7603	1	0.02	0.01	18.17	1252	278	32.59	58515	28296	25.38	10.20	0	312	0	0	572	0	0.00	0.00
CRC_Monitoring_162	60			PD	12-Jul-13	30-May-13	7.6	30-May-13	Qiagen	35053	Prevalence	TEMECT	0	9.98	8.01	14.70	0.12	1						14.70	10.03	0.12	0.50	14.69																	27.80		17.98	4024	882	11.41	2128	274	14.70	4.65	15.9	2753	521	4.15	28604	1239	10.03	8.31	0.23	1302	3	0	3520	0	0.12	0.16	0.31	20361	63	0.68	30488	210	0.50	0.26	6.15	397	26	23.23	228	69	14.69	12.08
CRC_Monitoring_162	60					28-Jun-13	18.8	28-Jun-13	Qiagen	9673	longitudinal	TEMECT	29	28.08	22.46	63.96	0.00	1						4.37	43.99	0.00	0.01	63.96																			4.37	438	20				4.37	3.09	48.7	3265	3099	39.27	16477	10655	43.99	6.67	0	529	0	0	1095	0	0.00	0.00	0	1344	0	0.01	9438	1	0.01	0.01	63.96	133	236				63.96	
CRC_Monitoring_162	60					26-Jul-13	24.1	26-Jul-13	Qiagen	10058	longitudinal	TEMECT	57	28.00	22.48	65.95	0.37	1						12.96	31.71	0.37	1.40	65.95																			3.25	3248	109	22.67	7073	2073	12.96	13.73	22.35	13033	3752	41.07	12735	8877	31.71	13.24	0.72	553	4	0.02	5187	1	0.37	0.49	0	16374	0	2.79	3549	102	1.40	1.97	68.97	279	620	62.92	89	151	65.95	4.28
CRC_Monitoring_163	66			SD	2-Apr-13	14-Feb-13	1.4	14-Feb-13	Qiagen	40107	Prevalence	TEMECT	0	1.39	0.68	2.12	0.00	1						0.13	0.52	0.00	0.65	2.12																	1.80		0	10704	0	0.26	2673	7	0.13	0.18	0	32265	12	1.03	22812	238	0.52	0.73	0	1668	0	0	4065	0	0.00	0.00	0.89	20599	186	0.41	30470	124	0.65	0.34	1.98	744	15	2.26	6761	156	2.12	0.20
CRC_Monitoring_163	66					15-Mar-13	1.2	15-Mar-13	Qiagen	12018	longitudinal	TEMECT	29	0.00	10.63	29.75	0.00	1						29.75	23.39	0.00	0.00	0.00																						23.78	1003	313	29.75	8.44	28.78	16048	6486	17.99	6908	1515	23.39	7.63	0	410	0	0	3204	0	0.00	0.00	0	1970	0	0	35469	1	0.00	0.00	0	733	0				0.00	
CRC_Monitoring_164	53			SD	28-Mar-13	18-Feb-13	517.2	18-Feb-13	Qiagen	75478	Prevalence	TEMECT	0	68.30	68.30	87.72	38.18	1						87.72	75.61	70.10	69.90	38.18																	69.70		82.59	2040	9680	92.84	523	6781	87.72	7.25	79.7	1201	4709	71.51	2843	7137	75.61	5.79	71.63	4893	12356	68.57	1508	3290	70.10	2.16	76.03	2362	7491	63.76	3284	5779	69.90	8.68	38.51	2178	1364	37.85	1128	687	38.18	0.47
CRC_Monitoring_164	53			PD	17-May-13	26-Mar-13	972.2	26-Mar-13	Qiagen	143352	longitudinal	TEMECT	36	0.16	0.16	0.61	0.00	0						0.00	0.15	0.03	0.03	0.61																			0	96539	1	0	38176	0	0.00	0.00	0.28	89780	248	0.02	95332	18	0.15	0.18	0.01	19238	2	0.04	108300	38	0.03	0.02	0.01	100940	8	0.05	238198	122	0.03	0.03	1.05	3206	34	0.16	619	1	0.61	0.63
CRC_Monitoring_164	53					22-Apr-13	1104	22-Apr-13	Qiagen	24994	longitudinal	TEMECT	63	55.57	55.57	99.99	32.18	1						48.19	57.16	99.99	32.18	40.34																			42.01	7437	5387	54.37	8682	10346	48.19	8.74	66.84	6493	13086	47.48	9995	9037	57.16	13.69	99.98	2	10000	100	0	124630	99.99	0.01	24.21	4061	1297	40.14	40287	27012	32.18	11.26	48.8	1063	1013	31.88	188	88	40.34	11.96
CRC_Monitoring_164	53					22-May-13	1412	22-May-13	Qiagen	29837	longitudinal	TEMECT	93	76.28	76.28	94.81	66.60	1						68.08	74.97	94.81	76.93	66.60																			75.28	202	615	60.87	2186	3401	68.08	10.19	81.82	985	4433	68.12	9159	19568	74.97	9.69	89.62	2191	18913	100	0	85313	94.81	7.34	87.36	2855	19739	66.5	29044	57660	76.93	14.75	59.16	214	310	74.04	61	174	66.60	10.52
CRC_Monitoring_165	61			PD	23-Jun-14	30-Apr-14	274.2	14-May-14	Qiagen	149959	Prevalence	TEMECT	0	73.99	73.99	90.03	39.53	1						76.23	77.07	90.03	87.11	39.53																	25.30		68.29	6518	14037	84.16	4387	23317	76.23	11.22	70.61	2989	7180	83.52	587	2975	77.07	9.13	88.07	357	2635	91.98	1992	22845	90.03	2.76	93.21	669	9177	81	4019	17129	87.11	8.63	42.02	2583	1872	37.04	2562	1507	39.53	3.52
CRC_Monitoring_165	61					11-Jun-14	830.2	11-Jun-14	Qiagen	241336	longitudinal	TEMECT	28	56.87	56.87	69.55	44.91	1						65.87	46.03	69.55	58.01	44.91																			65.97	9258	17945	65.77	11790	22652	65.87	0.14	44.47	17470	13988	47.58	14419	13090	46.03	2.20	67.52	11048	22972	71.57	2062	5190	69.55	2.86	59.33	8107	11825	56.69	27966	36607	58.01	1.87	44.95	2263	1848	44.86	2485	2022	44.91	0.06
CRC_Monitoring_165	61					4-Jul-14	2207	9-Jul-14	Qiagen	241646	longitudinal	TEMECT	56	72.54	72.54	96.63	50.29	1						76.54	69.45	96.63	69.81	50.29																			70.23	7169	16910	82.85	7097	34279	76.54	8.92	74.11	8806	25213	64.78	12432	22862	69.45	6.60	93.3	2801	38978	99.96	18	40529	96.63	4.71	77.86	3878	13639	61.75	23058	37228	69.81	11.39	46.98	615	545	53.6	6350	7336	50.29	4.68
CRC_Monitoring_166	39			PD	10-Jul-13	15-May-13	57.5	14-May-13	Qiagen	28811	Prevalence	TEMECT	0	22.58	9.12	31.71	0.00	1						0.42	0.02	0.00	31.71	13.44																	16.60		0.84	9436	80	0	4292	0	0.42	0.59	0	27892	5	0.03	53369	14	0.02	0.02	0	1658	0	0	4443	0	0.00	0.00	25.88	6544	2285	37.54	6406	3850	31.71	8.24	19.19	1415	336	7.69	276	23	13.44	8.13
CRC_Monitoring_166	39					24-May-13	63.7	24-May-13	Qiagen	36155	longitudinal	TEMECT	10	54.50	27.17	81.45	1.52	1						18.48	1.52	6.87	81.45	27.55																			11.14	5465	685	25.81	7779	2706	18.48	10.37	0.03	65398	21	3.01	12148	377	1.52	2.11	3.91	4109	167	9.82	32601	3550	6.87	4.18	79.81	4664	18441	83.08	846	4153	81.45	2.31	32.29	325	155	22.8	1243	367	27.55	6.71
CRC_Monitoring_167	53					28-May-13	73	28-May-13	Qiagen	13968	Prevalence	TEMECT	0	3.83	3.07	7.96	0.03	1						7.96	2.31	0.03	2.00	3.05																	0.00		15.92	4463	845	0	4353	0	7.96	11.26	0.1	9609	8	4.52	1688	80	2.31	3.13	0	6037	0	0.05	1849	1	0.03	0.04	3.99	17713	736	0	10161	0	2.00	2.82	3.18	945	31	2.91	734	22	3.05	0.19
CRC_Monitoring_168	72			PD	17-Apr-14	3-Mar-14	421.4	3-Mar-14	Qiagen	1210353	Prevalence	TEMECT	0	83.51	83.51	89.73	69.03	1						88.30	69.03	89.73	80.83	89.64																	81.00		91.4	3427	36444	85.2	4746	27331	88.30	4.38	64.8	1941	3566	73.26	671	1838	69.03	5.98	93.44	1264	18008	86.02	5095	31359	89.73	5.25	82.23	1412	6534	79.43	2875	11100	80.83	1.98	88.02	1094	8037	91.25	872	9090	89.64	2.28
CRC_Monitoring_168	72					29-Apr-14	1065	30-Apr-14	Qiagen	2267703	longitudinal	TEMECT	58	92.46	92.46	98.35	86.19	1						90.77	86.19	98.35	93.54	93.47																			86.41	2603	16554	95.12	2613	50919	90.77	6.16	82.11	3321	15241	90.27	4182	38778	86.19	5.77	98.1	1127	58183	98.59	1215	84958	98.35	0.35	93.06	2271	30448	94.01	5804	91171	93.54	0.67	94.42	970	16403	92.52	1145	14169	93.47	1.34
CRC_Monitoring_169	63			PD	21-Nov-13	2-Oct-13	342.8	2-Oct-13	Qiagen	306598	Prevalence	TEMECT	0	48.34	48.34	73.65	5.37	1						73.65	44.54	72.02	46.12	5.37																	19.80		79.94	4658	18562	67.36	7054	14560	73.65	8.90	36.9	2876	1679	52.18	3543	3866	44.54	10.80	71.63	1037	2618	72.41	1639	4302	72.02	0.55	42	2233	1617	50.23	2073	2092	46.12	5.82	6.34	8009	542	4.39	87822	4035	5.37	1.38
CRC_Monitoring_169	63							9-Oct-13	Qiagen	99536	longitudinal	TEMECT	7	48.49	48.49	85.05	6.25	1						85.05	43.70	57.62	49.82	6.25																			80.03	3083	12352	90.07	5914	53658	85.05	7.10	45.8	16651	14071	41.6	17036	12135	43.70	2.97	49.75	6805	6737	65.49	5639	10700	57.62	11.13	55.1	8196	10059	44.53	29248	23481	49.82	7.47	7.62	2618	216	4.88	18108	930	6.25	1.94
CRC_Monitoring_169	63					6-Nov-13	794.8	6-Nov-13	Qiagen	804444	longitudinal	TEMECT	35	65.55	65.55	94.77	8.55	1						90.06	65.41	94.77	68.96	8.55																			88.4	4879	37176	91.71	3757	41558	90.06	2.34	62.95	5362	9109	67.87	11437	24164	65.41	3.48	90.02	4113	37093	99.51	9	1814	94.77	6.71	70.99	4292	10503	66.93	17239	34897	68.96	2.87	10.93	1280	157	6.16	34987	2297	8.55	3.37
CRC_Monitoring_169	63					5-Dec-13	1144	5-Dec-13	Qiagen	1549740	longitudinal	TEMECT	64	74.26	74.26	98.98	9.34	1						88.46	84.11	98.98	90.42	9.34																			83.6	4057	20676	93.32	2568	35855	88.46	6.87	82.54	4245	20064	85.68	5414	32382	84.11	2.22	97.95	1307	62319	100	0	8966	98.98	1.45	91.17	1700	17549	89.67	6692	58079	90.42	1.06	10.35	8073	932	8.32	41411	3759	9.34	1.44
CRC_Monitoring_170	74					16-Dec-13	51.6	19-Dec-13	Qiagen	29333	Prevalence	TEMECT	0		0.04	0.10	0.00	0						0.00	0.09	0.00	0.00	0.10																	0.00		0	6942	0	0	7114	0	0.00	0.00	0.1	24273	13	0.07	5493	4	0.09	0.02	0	1042	0	0	3483	0	0.00	0.00	0	26986	1	0	31310	0	0.00	0.00	0.19	516	1	0	477	0	0.10	0.13

Supplementary File 2H

Association between clinico-pathological features and circulating DNA methylation

		Median	pvalue
Sex	Female	35.60	***0.029***
	Male	11.80	
Age (years)	[33-54.7[	23.25	*ns*
	[54.7-62.9[	12.80	
	[62.9-72.7[	12.40	
	[72.7-85.2]	17.85	
CEA (ng/ml)	<=5	2.80	*ns*
	>5	18.60	
RECIST (mm)	[9-49.25[	3.15	*ref.*
(quartiles)	[49.25-81.55[	17.10	***0.06***
	[81.55-117[	18.10	*ns*
	[117-250]	33.80	***0.006***
GE/ml	[1110-19613[	2.40	*ref.*
(quartiles)	[19613-40107[	10.10	*ns*
	[40107-137394[	34.20	***<0.001***
	[137394-9259908]	69.95	***<0.001***
Primary tumor intact	No	12.45	***0.002***
	Yes	53.20	
Metastatic lesions	1	5.50	***0.023***
	2+	22.45	
Bulky disease	No	11.85	***0.012***
	Yes	39.00	
RAS	wild type	15.60	*ns*
	mutated	17.80	
BRAF	wild type	15.70	*ns*
	mutated	47.40	
Under treatment	No	18.35	*ns*
	Yes	14.20	

Supplementary File 2I

Case_ID	Collection_Date	Days	Average marker>1% in BL	Mn-M0	Best_CH3_change	Date CT Scan	Days to plasma baseline	Days to closest blood draw	SUM target lesions	PD x new lesions (y/n)	RECIST_Change	BEST_RECIST	CEA	PFS	Best_response (0:PD; 1:SD; 2:PR)	MGMT Methylation at baseline
CRC_Monitoring_142	28-Dec-12	0	34.5	0.0		4-Dec-12	-24	-24	141	0			164	2.80	1	42.9
CRC_Monitoring_142	9-Jan-13	12	19.7	-14.8	x								107.3	2.80	1	42.9
CRC_Monitoring_142	25-Jan-13	28	50.3	15.7		8-Feb-13	42	14	137		-2.8	X	197.4	2.80	1	42.9
CRC_Monitoring_142	20-Feb-13	54	47.6	13.0									150.4	2.80	1	42.9
CRC_Monitoring_142	1-Mar-13	63	38.0	3.4		22-Mar-13	84	21	152	y	7.8		209.4	2.80	1	42.9
CRC_Monitoring_143	25-Jan-13	0	51.4	0.0		23-Jan-13	-2	-2	117	n			44.5	2.77	1	44.3
CRC_Monitoring_143	14-Feb-13	20	3.8	-47.7									30.3	2.77	1	44.3
CRC_Monitoring_143	20-Feb-13	26	0.2	-51.3	x								32.5	2.77	1	44.3
CRC_Monitoring_143	4-Mar-13	38	5.8	-45.7		8-Mar-13	42	4	97		-17.1	X	48.5	2.77	1	44.3
CRC_Monitoring_143	27-Mar-13	61	54.2	2.8									92.1	2.77	1	44.3
CRC_Monitoring_143	23-Apr-13	88	68.0	16.6		19-Apr-13	84	-4	119		1.7		115.6	2.77	1	44.3
CRC_Monitoring_144	23-Aug-13	0	2.3	0.0		6-Aug-13	-17	-17	97	0			13.3	4.30	1	14.6
CRC_Monitoring_144	23-Oct-13	61	13.6	11.4	x	10-Oct-13	48	-13	95		-2.1	X	29.3	4.30	1	14.6
CRC_Monitoring_144	18-Dec-13	117	62.7	60.4		20-Nov-13	89	-28	102		5.2		22	4.30	1	14.6
CRC_Monitoring_144	27-Jan-14	157	72.7	70.4		3-Jan-14	133	-24	99	y	2.1		25.7	4.30	1	14.6
CRC_Monitoring_145	19-Dec-13	0	2.0	0.0		20-Dec-13	1	1	84	0			80	1.37	0	0.0
CRC_Monitoring_145	22-Jan-14	34	1.2	-0.7	x	3-Feb-14	46	12	100	y	19	X	117.9	1.37	0	0.0
CRC_Monitoring_146	5-Jul-13	0	15.6	0.0		10-Jul-13	5	5	126	n			147.6	2.77	1	0.0
CRC_Monitoring_146	8-Aug-13	34	40.5	24.9	x	21-Aug-13	47	13	146		15.9	X	238.1	2.77	1	0.0
CRC_Monitoring_146	5-Sep-13	62	52.1	36.6									309.1	2.77	1	0.0
CRC_Monitoring_146	12-Sep-13	69	84.0	68.4									334.5	2.77	1	0.0
CRC_Monitoring_146	10-Oct-13	97	61.7	46.1		3-Oct-13	90	-7	165		31		592.3	2.77	1	0.0
CRC_Monitoring_147	3-Sep-13	0	29.3	0.0		3-Aug-13	-31	-31	133	0			112.9	2.87	1	4.0
CRC_Monitoring_147	2-Oct-13	29	2.2	-27.2	x	15-Oct-13	42	13	127		-4.5		52.3	2.87	1	4.0
CRC_Monitoring_147	30-Oct-13	57	2.2	-27.1		29-Nov-13	87	30	105	y	-21.1	X	16.6	2.87	1	4.0
CRC_Monitoring_148	21-Jan-13	0	77.8	0.0		21-Jan-13	0	0	135	n			3389	1.37	0	61.9
CRC_Monitoring_148	11-Feb-13	21	88.2	10.5	x	11-Mar-13	49	28	163	y	20.7	X	3440	1.37	0	61.9
CRC_Monitoring_149	14-Jan-13	0	12.8	0.0		21-Dec-12	-24	-24	167	n			1866	1.63	0	9.7
CRC_Monitoring_149	11-Feb-13	28	27.3	14.6	x								2148	1.63	0	9.7
CRC_Monitoring_149	8-Mar-13	53	49.3	36.6		6-Mar-13	51	-2	194	y	16.2	X	2446	1.63	0	9.7
CRC_Monitoring_151	6-May-13	0	72.7	0.0		6-May-13	0	0	53	0			11	1.30	0	69.3
CRC_Monitoring_151	7-Jun-13	32	84.5	11.8	x	21-Jun-13	46	14	92		73.6	X	21.6	1.30	0	69.3
CRC_Monitoring_151	5-Jul-13	60	88.9	16.2									52.7	1.30	0	69.3
CRC_Monitoring_152	14-Mar-13	0	37.4	0.0		11-Mar-13	-3	-3	34	n			19.2	2.77	1	0.0
CRC_Monitoring_152	26-Mar-13	12	13.3	-24.1	x								21.5	2.77	1	0.0
CRC_Monitoring_152	24-Apr-13	41	14.8	-22.6		8-May-13	55	14	34		0	X	40	2.77	1	0.0
CRC_Monitoring_152	22-May-13	69	40.2	2.9		18-May-13	65	-4	45	y	32.4		41.7	2.77	1	0.0
CRC_Monitoring_152	20-Jun-13	98	58.8	21.4									119.9	2.77	1	0.0
CRC_Monitoring_153	21-Mar-13	0	80.6	0.0		12-Mar-13	-9	-9	57	n			84.1	5.43	2	74.2
CRC_Monitoring_153	3-May-13	43	71.2	-9.3		3-May-13	43	0	40		-29.8		176.7	5.43	2	74.2
CRC_Monitoring_153	4-Jun-13	75	57.1	-23.5	x	4-Jun-13	75	0	40		-29.8	X	246.9	5.43	2	74.2
CRC_Monitoring_153	27-Jun-13	98	88.9	8.3		27-Jun-13	98	0	43		-24.6		449	5.43	2	74.2
CRC_Monitoring_153	4-Sep-13	167	87.0	6.4		4-Sep-13	167	0	69		21.1		1073	5.43	2	74.2
CRC_Monitoring_154	25-Jan-13	0	16.4	0.0		29-Jan-13	4	4	105	n			496.9	1.50	0	17.0
CRC_Monitoring_154	25-Feb-13	31	42.3	25.9	x	15-Mar-13	49	18	121	y	15.2	X	666.8	1.50	0	17.0
CRC_Monitoring_154	26-Mar-13	60	57.7	41.3									789.3	1.50	0	17.0
CRC_Monitoring_155	3-Apr-13	0	35.6	0.0		8-Apr-13	5	5	107	n			634.7	2.47	0	21.1
CRC_Monitoring_155	11-Apr-13	8	63.2	27.7	x									2.47	0	21.1
CRC_Monitoring_155	9-May-13	36	65.3	29.7									1629	2.47	0	21.1
CRC_Monitoring_156	10-Apr-13	0	0.8	0.0		12-Apr-13	2	2	29	n			68.4	1.43	0	0.0
CRC_Monitoring_156	30-Apr-13	20	1.8	1.0	x								80.6	1.43	0	0.0
CRC_Monitoring_156	28-May-13	48	16.7	15.9									104.7	1.43	0	0.0
CRC_Monitoring_156	2-Jul-13	83	38.7	37.9		12-Jun-13	63	-20	36		24.1	X	111.5	1.43	0	0.0
CRC_Monitoring_158	28-Feb-14	0	14.6	0.0		10-Feb-14	-18	-18	29	n			6.8	1.63	1	57.8
CRC_Monitoring_158	27-Mar-14	27	0.0	-14.6	x	8-Apr-14	39	12	26		-10.3	X	3.11	1.63	1	57.8
CRC_Monitoring_158	7-May-14	68	5.2	-9.4									2.85	1.63	1	57.8
CRC_Monitoring_158	21-May-14	82	0.8	-13.8		20-May-14	81	-1	32		10.3		11.2	1.63	1	57.8
CRC_Monitoring_158	25-Jun-14	117	0.0	-14.6									23	1.63	1	57.8
CRC_Monitoring_159	17-Dec-13	0	17.8	0.0		18-Dec-13	1	1	172	n			262.8	1.40	0	8.8
CRC_Monitoring_159	22-Jan-14	36	36.2	18.4	x	3-Feb-14	48	12	198	y	15.1	X	373	1.40	0	8.8
CRC_Monitoring_159	19-Feb-14	64	45.2	27.3									523.4	1.40	0	8.8
CRC_Monitoring_160	18-Feb-14	0	47.4	0.0		5-Feb-14	-13	-13	107	n			280	10.63	1	0.0
CRC_Monitoring_160	20-Mar-14	30	46.7	-0.7	x								370.9	10.63	1	0.0
CRC_Monitoring_160	17-Apr-14	58	55.6	8.2		4-Apr-14	45	-13	126		17.8	X	659.4	10.63	1	0.0
CRC_Monitoring_161	4-Mar-14	0	4.5	0.0		26-Feb-14	-6	-6	29	n			22	2.83	1	0.6
CRC_Monitoring_161	9-Apr-14	36	16.1	11.6		23-Apr-14	50	14	24		-17.2	X	37.4	2.83	1	0.6
CRC_Monitoring_161	7-May-14	64	13.4	8.9	x	30-May-14	87	23	31	y	6.9		47.6	2.83	1	0.6
CRC_Monitoring_162	30-May-13	0	10.0	0.0		2-May-13	-28	-28	79	n			7.6	1.40	0	27.8
CRC_Monitoring_162	28-Jun-13	29	28.1	18.1	x								18.8	1.40	0	27.8
CRC_Monitoring_162	26-Jul-13	57	28.0	18.0		12-Jul-13	43	-14	108		36.7	X	24.1	1.40	0	27.8
CRC_Monitoring_163	14-Feb-13	0	1.4	0.0		23-Jan-13	-22	-22	190	n			1.4	4.00	1	1.8
CRC_Monitoring_163	15-Mar-13	29	0.0	-1.4	x	2-Apr-13	47	18	194		2.1	X	1.2	4.00	1	1.8
CRC_Monitoring_164	18-Feb-13	0	68.3	0.0		20-Feb-13	2	2	142	n			517.2	2.80	1	69.7
CRC_Monitoring_164	26-Mar-13	36	0.2	-68.1	x	28-Mar-13	38	2	140		-1.4	X	972.2	2.80	1	69.7
CRC_Monitoring_164	22-Apr-13	63	55.6	-12.7									1104	2.80	1	69.7
CRC_Monitoring_164	22-May-13	93	76.3	8.0		17-May-13	88	-5	152	y	7		1412	2.80	1	69.7
CRC_Monitoring_165	14-May-14	0	74.0	0.0		14-May-14	0	0	147				274.2	1.30	0	25.3
CRC_Monitoring_165	11-Jun-14	28	56.9	-17.1	x	23-Jun-14	40	12	176		19.7	X	830.2	1.30	0	25.3
CRC_Monitoring_165	9-Jul-14	56	72.5	-1.5						n			2207	1.30	0	25.3
CRC_Monitoring_166	14-May-13	0	22.6	0.0		23-May-13	9	9	48				57.5	1.57	0	16.6
CRC_Monitoring_166	24-May-13	10	54.5	31.9	x	10-Jul-13	57	47	79		64.6	X	63.7	1.57	0	16.6
CRC_Monitoring_168	3-Mar-14	0	83.5	0.0		5-Feb-14	-26	-26	85				421.4	1.40	0	81.0
CRC_Monitoring_168	30-Apr-14	58	92.5	9.0	x	17-Apr-14	45	-13	117	y	37.6	X	1065	1.40	0	81.0
CRC_Monitoring_169	2-Oct-13	0	48.3	0.0		4-Oct-13	2	2	108	n			342.8	1.40	0	19.8
CRC_Monitoring_169	9-Oct-13	7	48.5	0.1	x									1.40	0	19.8
CRC_Monitoring_169	6-Nov-13	35	65.6	17.2									794.8	1.40	0	19.8
CRC_Monitoring_169	5-Dec-13	64	74.3	25.9		21-Nov-13	50	-14	135	y	25	X	1144	1.40	0	19.8

Supplementary File 3

Experimental design	
Definition of experimental and control groups:	Marker Discovery (From microarrays on tissue, new data and publically available dataset): Identification of markers: Cell bank (GSE86078; N=149) Normal Mucosa (GSE32146; N=20) Blood controls (GSE41169; N=34) In-silico Validation: Test set (GSE72752; N=63) Validation set (TCGA COREAD; N=446 / GSE48684; N=41) Tissue validation: Normal / matched cohort (N=32) Plasma matched cohort (N=51) cfDNA assessment: Prevalence assessment § Aging cohort, self-declared healthy (N=50) § mCRC cohort (N=135) § Longitudinal cohort – baselines (N=47) Longitudinal assessment: § Conventional chemotherapies (N=12) § Targeted therapy (N=6) § Clinical trial with temozolomide (N=29) All Cohorts and numbers are also reported in Figure 1.
Assay carried out by core lab or investigator's lab?	All experiments were carried out in the investigator's laboratory. All DNA extraction and subsequent molecular characterization were carried out at the Department of Oncology of the Univesity of Turin."
Sample Description	
Samples used	Description and annotation of samples can be found in supplementary data 1A for the microarray analyses and in supplementary data 1E for the tissue and cfDNA samples.
Volume or mass of sample processed.	Concerning the FFPE samples: § the normal / tumor matched samples were macrodissected and a piece of FFPE block (~9mm3) was sent to the laboratory for extraction. § the plasma matched tissues were remaining DNA samples extracted from two 10um slides (without tumour cellularity control) extracted using the QIA FFPE tissue kit (Qiagen). Concerning the cfDNA: One or two 6ml vacutainer tubes were collected from each timepoint of the CRC cohorts. Blood were processed within six hours as previously described (two steps centrifugation), and aliquoted into 1ml cryovials which were stored at -80°C until DNA extraction. These samples being used for collaborative project one milliliter of plasma was available for the current study.
Microdissection or macrodissection.	the normal / tumor matched samples were macrodissected. While FFPE tissue DNA (plasma matched tumours) were obtained through a previous project in which only the tumor extension was controlled without further dissection.

Processing procedure	
If frozen—how and how quickly?	Plasma samples from CRC patients were frozen at -80°C within six hours after collection.
If fixed—with what, how quickly?	Fixation was performed in Paraformaldehyde 4%.Since tissue samples were retrieved from multiple collection center across Italie, it was not possible to retrieve the exact fixation duration period
Sample storage conditions and duration	- FFPE block were from archival tissue bank and have been stored between at room temperature in darkness up to 13 years prior processing (average=6 years). Cut of the block was performed prior to DNA extraction. - Plasma samples were kept at -80°C prior to extraction up to 8 years (average = 4 years).
Nucleic acid extraction	
Quantification—instrument/method.	- FFPE tissue DNA were quantified using Nanodrop system. - Circulating DNA were quantified by genome equivalent evaluated by qPCR using the LINE1 assay previously described in Siravegna et al. Nat Med. 2015.
Storage conditions: temperature, concentration, duration, buffer.	- All native / concentrated DNA were eluted in water and stored at +4°C.
Template structural information.	DNA were from FFPE tissue origin or from cell free circulating DNA. DNA were stored without further modifications prior to their bisulfite conversion for methylation analyses.
Template modification (digestion, sonication, preamplification, etc.).	Template were bisulfite converted as mentioned in material and methods using the EZ methylation Gold kit from Zymo Research according to manufacturers' procedure except for the elution step which was carried out in twice 20ul for cfDNA and in twice 40ul for tissue DNA.
Manufacturer of reagents used and catalogue number	- Qiagen - QIAamp DNA FFPE Tissue Kit - Cat No./ID: 56404 - Qiagen - QIAamp Circulating Nucleic Acid Kit - Cat No./ID: 55114 - Promega - Maxwell® RSC ccfDNA Plasma Kit - Cat No./ID:AS1480 - Zymo Research - EZ DNA Methylation-Gold™ Kit - Cat No./ID: D5006
Reaction volume	- Bisulfite conversion was carried out as follow: §FFPE DNA : input : 250ng output: 2x40ul §cfDNA : input: 20ul output: 2x20ul - 1st PCR amplification: FFPE and cfDNA : input : 2ul of bisulfite converted DNA per reaction final volume: 20ul - 2nd amplification (EmPCR): FFPE : Input : 3.5ul of 1st amplification (diluted at 1/20000) final volume: 20ul (+70ul oil) cfDNA : Input : 3.5ul of 1st amplification (diluted at 1/6000) final volume: 20ul (+70ul oil)

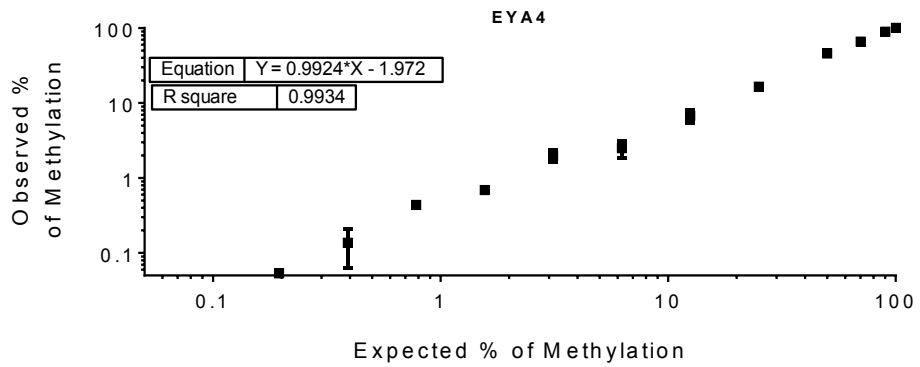
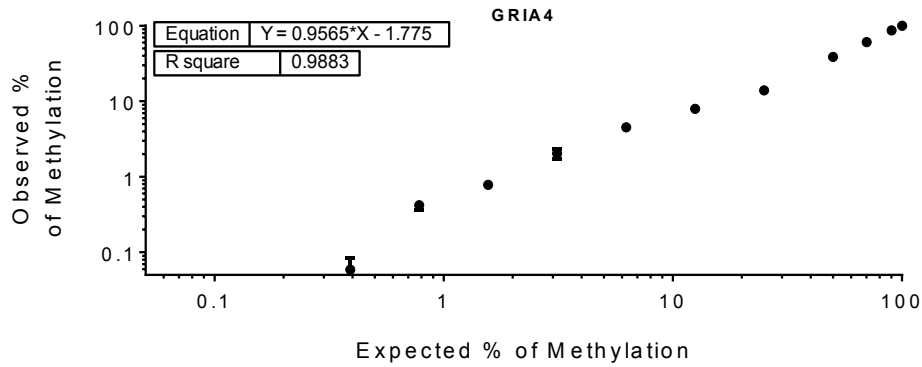
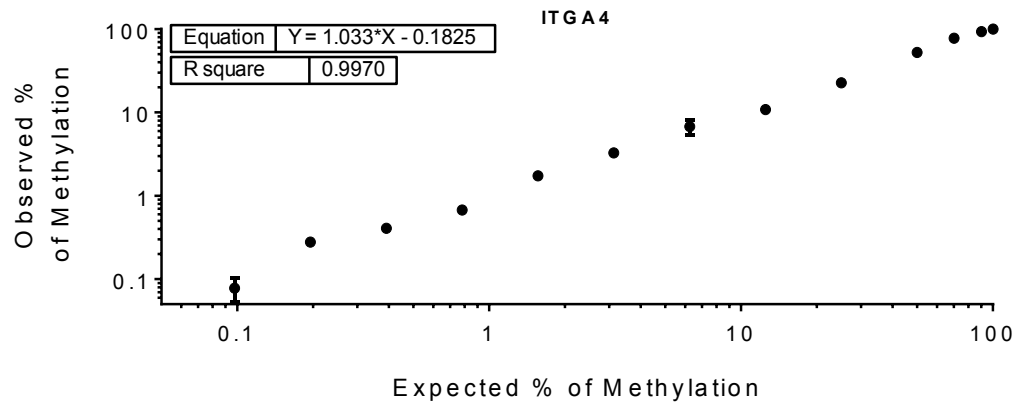
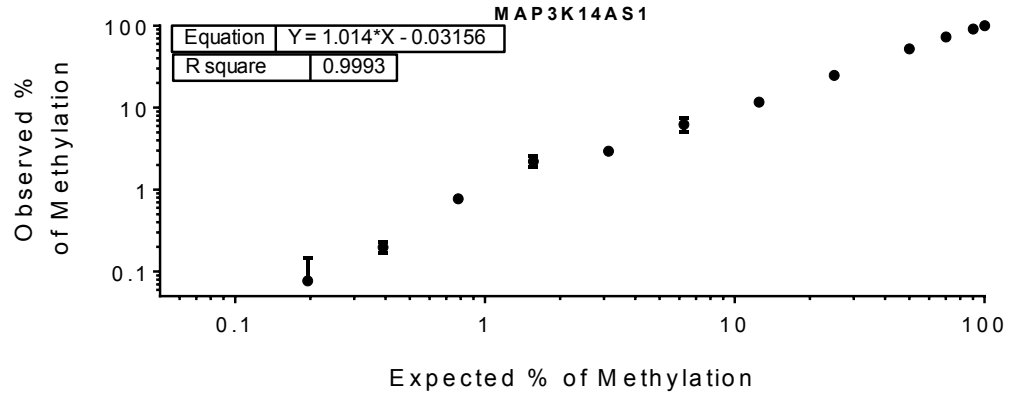
dPCR target information	
Amplicon length	C9orf50: 114bp EYA4: 96bp GRIA4: 106bp ITGA4: 76bp MAP3K14-AS1: 99bp MSC: 122bp SEPT9: 75bp
In silico specificity screen (BLAST, etc.)	- ***EYA4:*** **PCR product(s) on the bisulfite transformed sense chain** Forward primer: GTGGATAGGATGGAAGTTT Reverse primer: CCCCCCCCACCTCCCTAC No PCR product should be generated. **PCR product(s) on the bisulfite transformed antisense chain** Forward primer: GTGGATAGGATGGAAGTTT Reverse primer: CCCCCCCCACCTCCCTAC 1. Chromosome 6 (len: 96) 133241282 CCCAC CCCACCTCCC TACACAAATA CAAAACTACC AACAACACAA CACACACTCC AACCATTCCC AACTTCCACA CAAAACTTCC ATCCTATCCA C 133241378 - ***GRIA4:*** **PCR product(s) on the bisulfite transformed sense chain** Forward primer: GGGTTGGTGTAGGTTTGTT Reverse primer: CTCCCCCCTTACTTTCTCACATACACACAA 1. Chromosome 11 (len: 106) 105610527 GG GTTGGTGTAG GTTTGTTGGG GGATGTTGGT TGATGTGAGT TGGAGAGTGT GTGTGGTGGT TGTGGTGTTA GTGTTTGTGT GTATGTGAGA AAGTAAGGGG TGAG 105610633 **PCR product(s) on the bisulfite transformed antisense chain** Forward primer: GGGTTGGTGTAGGTTTGTT Reverse primer: CTCCCCCCTTACTTTCTCACATACACACAA No PCR product should be generated. - ***ITGA4:*** **PCR product(s) on the bisulfite transformed sense chain** Forward primer: GGGGAAGAAAGTTTTAAGAGATGAG Reverse primer: TCCTCTTCCCTCTCTCCT No PCR product should be generated. **PCR product(s) on the bisulfite transformed antisense chain** Forward primer: GGGGAAGAAAGTTTTAAGAGATGAG Reverse primer: TCCTCTTCCCTCTCTCCT 1. Chromosome 2 (len: 76) 181457503 T CCTCTTCCCT CTCTCCTTCC TTTAACCCAC TAACACCAAA CACACTACAC CTCATCTCTT AAAACATTCT TCCCC 181457579 - ***MAP3K14-AS1:*** **PCR product(s) on the bisulfite transformed sense chain** Forward primer: GGATTGGTGGGAGTTGGAAATATTAGA Reverse primer: ACCTAAATACCACTCCCTACCTATAAAAT 1. Chromosome 17 (len: 103) 45262097 GGATTG GTGGGTGTTG GAAATATTAG AGGTGTTGGT GTTTGTGATG TTGTTGTTTT TGTGATGTTT TTGTTGTGAT TTTATAGGTA GGGAGTTGTA TTTAGGT 45262200 **PCR product(s) on the bisulfite transformed antisense chain** Forward primer: GGATTGGTGGGAGTTGGAAATATTAGA Reverse primer: ACCTAAATACCACTCCCTACCTATAAAAT No PCR product should be generated.

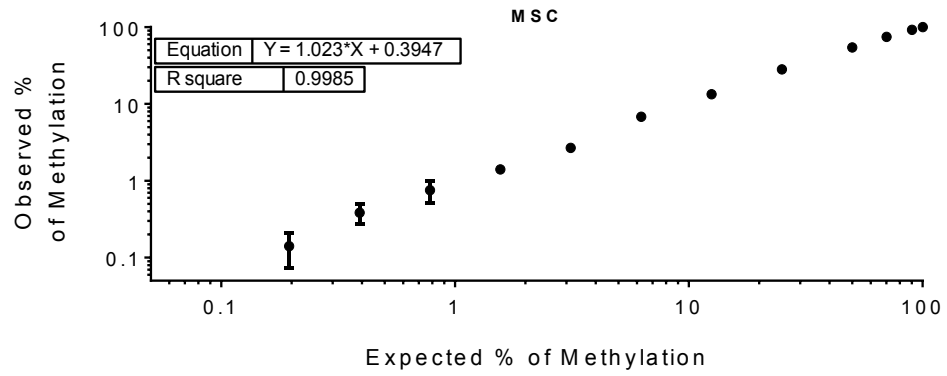
	- ***MSC:*** **PCR product(s) on the bisulfite transformed sense chain** Forward primer: **AGGGTTTAGTAGTAGAGTGTAAGT** Reverse primer: **AAACACCCAAAACAAACTAATCT** No PCR product should be generated. **PCR product(s) on the bisulfite transformed antisense chain** Forward primer: **AGGGTTTAGTAGTAGAGTGTAAGT** Reverse primer: **AAACACCCAAAACAAACTAATCT** 1. **Chromosome 8** (len: 122) 71843764 **AAA CACCCAAAAC** **AAACTAATCT** TAAACCTAAA AAAAACTTTA CTCAACACAC ACATCCAAAC ACACTCACAA ACATTAACCA CATTCCACTA CAACT**ACTTA CACTCTAC**A**A** **CTAAACCCT** 71843886
Pseudogenes, or other homologs	Not found.
Secondary structure analysis of amplicon and GC content.	- ***EYA4 amplicon:*** **SEQUENCE** 5'- CCC ACC TCC CTA CAC AAA TAC AAA ACT ACC AAC AAC ACA ACA CAC ACT CCA ACC ATT CCC AAC TTC CAC ACA AAA CTT CCA TCC TAT CCA C -3' **COMPLEMENT** 5'- GTG GAT AGG ATG GAA GTT TTG TGT GGA AGT TGG GAA TGG TTG GAG TGT GTG TTG TGT TGT TGG TAG TTT TGT ATT TGT GTA GGG AGG TGG G -3' LENGTH 91 GC CONTENT 45.1 % MELT TEMP 71 ºC MOLECULAR WEIGHT 27328.8 g/mole EXTINCTION COEFFICIENT 856400 L/(mole·cm) nmole/OD260: 1.17 µg/OD260: 31.91 - ***GRIA4 amplicon:*** **SEQUENCE** 5'- GGG TTG GTG TAG GTT TGT TGG GGG ATG TTG GTT GAT GTG AGT TGG AGA GTG TGT GTG GTG GTT GTG GTG TTA GTG TTT GTG TGT ATG TGA GAA AGT AAG GGG TGA G -3' **COMPLEMENT** 5'- CTC ACC CCT TAC TTT CTC ACA TAC ACA CAA ACA CTA ACA CCA CAA CCA CCA CAC ACA CTC TCC AAC TCA CAT CAA CCA ACA TCC CCC AAC AAA CCT ACA CCA ACC C -3' LENGTH 106 GC CONTENT 48.1 % MELT TEMP 71.9 ºC MOLECULAR WEIGHT 33593.6 g/mole EXTINCTION COEFFICIENT 1053700 L/(mole·cm) nmole/OD260: 0.95 µg/OD260: 31.88 - ***ITGA4 amplicon:*** **SEQUENCE** 5'- TCC TCT TCC CTC TCT CCT TCC TTT AAC CCA CTA ACA CCA AAC ACA CTA CAC CTC ATC TCT TAA AAC ATT CTT CCC C -3' **COMPLEMENT** 5'- GGG GAA GAA TGT TTT AAG AGA TGA GGT GTA GTG TGT TTG GTG TTA GTG GGT TAA AGG AAG GAG AGA GGG AAG AGG A -3' LENGTH 76 GC CONTENT 44.7 % MELT TEMP 69.8 ºC MOLECULAR WEIGHT 22717.8 g/mole EXTINCTION COEFFICIENT 669200 L/(mole·cm) nmole/OD260: 1.49 µg/OD260: 33.95

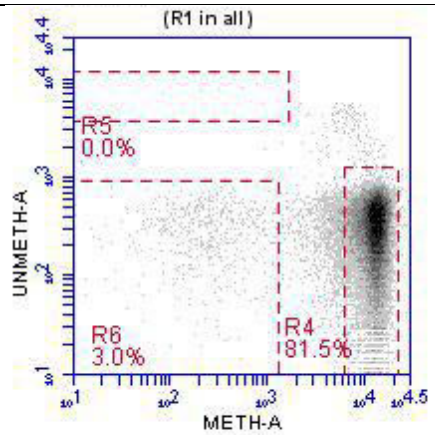
	- ***MAP3K14-AS1 amplicon:*** **SEQUENCE** 5'- GGA TTG GTG GGT GTT GGA AAT ATT AGA GGT GTT GGT GTT TGT GAT GTT GTT GTT TTT GTG ATG TTT TTG TTG TGA TTT TAT AGG TAG GGA GTT GTA TTT AGG T -3' **COMPLEMENT** 5'- ACC TAA ATA CAA CTC CCT ACC TAT AAA ATC ACA ACA AAA ACA TCA CAA AAA CAA CAA CAT CAC AAA CAC CAA CAC CTC TAA TAT TTC CAA CAC CCA CCA ATC C -3' LENGTH 103 GC CONTENT 35.9 % MELT TEMP 70 ºC MOLECULAR WEIGHT 32339.9 g/mole EXTINCTION COEFFICIENT 1005700 L/(mole·cm) nmole/OD260: 0.99 µg/OD260: 32.16 - ***MSC amplicon:*** **SEQUENCE** 5'- AAA CAC CCA AAA CAA ACT AAT CTT AAA CCT AAA AAA AAC TTT ACT CAA CAC ACA CAT CCA AAC ACA CTC ACA AAC ATT AAC CAC ATT CCA CTA CAA CTA CTT ACA CTC TAC AAC TAA ACC CT -3' **COMPLEMENT** 5'- AGG GTT TAG TTG TAG AGT GTA AGT AGT TGT AGT GGA ATG TGG TTA ATG TTT GTG AGT GTG TTT GGA TGT GTG TGT TGA GTA AAG TTT TTT TTA GGT TTA AGA TTA GTT TGT TTT GGG TGT TT -3' LENGTH 122 GC CONTENT 33.6 % MELT TEMP 70.6 ºC MOLECULAR WEIGHT 36957.2 g/mole EXTINCTION COEFFICIENT 1201200 L/(mole·cm) nmole/OD260: 0.83 µg/OD260: 30.77
dPCR oligonucleotides	
Primer sequences	- **C9orf50:** FW [TCCCGCGAAATTAATACGAC]ATTTAAGGAATTTGTTGGGGAGGA RV [GCTGGAGCTCTGCAGCTA]CCCAAACAACCAAAACCTAA - **EYA4:** FW [TCCCGCGAAATTAATACGAC]GTGGATAGGATGGAAGTTT RV [GCTGGAGCTCTGCAGCTA]CCCCCCCCACCTCCCTAC - **GRIA4:** FW [TCCCGCGAAATTAATACGAC]GGGTTGGTGTAGGTTTGTT RV [GCTGGAGCTCTGCAGCTA]CTCCCCCCTTACTTTCTCACATACACACAA - **ITGA4** FW [TCCCGCGAAATTAATACGAC]GGGGAAGAAAGTTTTAAGAGATGAG RV [GCTGGAGCTCTGCAGCTA]TCCTCTTCCCTCTCTCCT - **MAP3K14-AS1:** FW [TCCCGCGAAATTAATACGAC]GGATTGGTGGGAGTTGGAAATATTAGA RV [GCTGGAGCTCTGCAGCTA]ACCTAAATACCACTCCCTACCTATAAAAT - **MSC:** FW [TCCCGCGAAATTAATACGAC]AGGGTTTAGTAGTAGAGTGTAAGT RV [GCTGGAGCTCTGCAGCTA]AAACACCCAAAACAAACTAATCT - **SEPT9:** FW [TCCCGCGAAATTAATACGAC]GGATTTAGAAGGTGGGTGTTGG RV [GCTGGAGCTCTGCAGCTA]CCAAACCCACCCCCAAAATCCTCTC
Probe sequences	- **C9orf50** Metylated-Probe /5Alex647N/AACGCGAACGCCCCCGAA Unmethylated-Probe /5Alex488N/AACACAAACACCCCCAAA - **EYA4** Metylated-Probe /5Alex647N/GACCGTTCCCGACTTCCGC Unmetylated-Probe /5Alex488N/CACTCCAACCATTCCCA - **GRIA4** Metylated-Probe /5Alex647N/AACGCCGCGACCGCCACAC

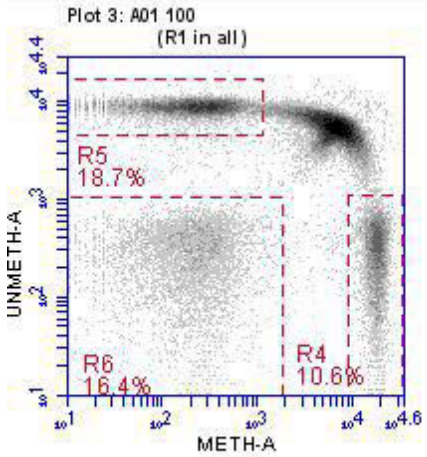
	Unmetylated-Probe /5Alex488N/CACCACAACCACCACACACA - **ITGA4** Metylated-Probe /5Alex647N/ACCCGCTAACGCCGAACACGCTA Unmetylated-Probe /5Alex488N/ACCCACTAACACCAAACACACTA - **MAP3K14-AS1** Metylated-Probe /5Alex647N/CGACGACATCACAAACACCGACG Unmetylated-Probe /5Alex488N/CAACAACATCACAAACACCAACA - **MSC** Metylated-Probe /5Alex647N/CGCATCCGAACACGCTCAC Unmetylated-Probe /5Alex488N/ACACATCCAAACACACTCAC - **SEPT9** Metylated-Probe /5Alex647N/CCGCGACCGCAACAACC Unmetylated-Probe /5Alex488N/CCACAACCACAACAACC
Manufacturer of oligonucleotides	All primers and probes were ordered through IDT.
Purification method	Primers were ordered desalted while probes were purified with HLPC and modified with fluorescent dye at 5' (/5Alex647N/ for methylated probe ; /5Alex488N/ for unmethylated probes)
dPCR protocol	
Complete reaction conditions	**- Mg concentrations:** - C9orf50: 1.5mM - EYA4: 2 mM - GRIA4: 1.5 mM - ITGA4: 2.5 mM - MAP3K14-AS1: 2.5 mM - MSC: 1.5 mM - SEPT9: 1 mM **- Tm:** - C9orf50: 50°C - EYA4: 54°C - GRIA4: 62°C - ITGA4: 50°C - MAP3K14-AS1: 50°C - MSC: 58°C - SEPT9: 56°C
Plates/tubes Catalogue No and manufacturer	-1 1st amplification: 8-tube strips for qPCR with individually attached, optically clear, flat caps (VWR – Cat No: 211-0338) - EmPCR: PCR-PLATE 96-WELL NON-SKIRTED STP (VWR – Cat No: 732-2387)
Complete thermocycling parameters.	- **1st amplification:** 94°C 2 min ----- Θ ---- 94°C 30 sec Tm 15 sec Tm:see above 72°C 15 sec -- go to Θ -- x39 72°C 5 min - **EmPCR amplification:** 94.0 2 min ----- ① ---- 94.0 10 sec 68.0 50 sec 70.0 80 sec

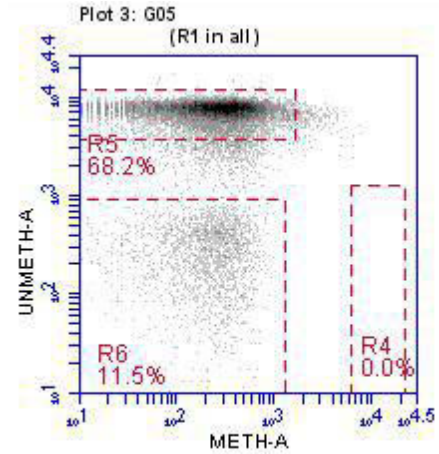
	-- go to ① -- x3 ----- ② ---- 94.0 10 sec 65.0 50 sec 70.0 80 sec -- go to ② -- x3 ----- ③ ---- 94.0 10 sec 62.0 50 sec 70.0 80 sec -- go to ③ -- x3 ----- ④ ---- 94.0 10 sec 59.0 50 sec 70.0 80 sec -- go to ④ -- x50 70.0 2 min
Reaction setup	Buffer, Magnesium and Taq are from Platinum® Taq DNA Polymerase (ref. Thermo Fisher 10966018) dNTP are from dNTP Set (100 mM) (ref. Thermo Fisher 10297018) - **1st amplification:** Buffer: 1X Mg: See above dNTP: 300nM primers: 200nM Taq: 0.75 unit Template : 2 ul (variable concentration) H2O: qsp 20 ul - **EmPCR (Ref: Diehl 2006, Nat methods):** Buffer: 1X Mg: 5 mM dNTPs: 200uM Tag 2: 8 uM Tag1: 50 nM Beads: 6.107 Taq Platinum: 2 units DNA: ~25 pg H2O: qsp 20 ul
Manufacturer of instrument	Amplification performed on a Bio-rad C1000 thermocycler. Reading was performed on a BD – Accuri C6 flow cytometer.

Optimization data for the assay	   

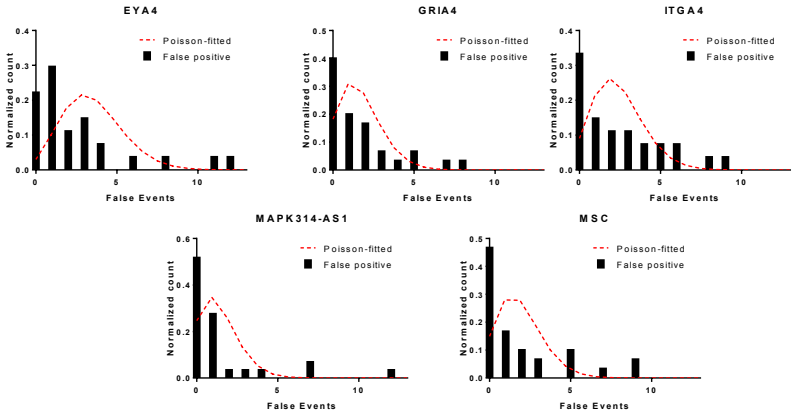
	
Limit of detection of calibration control.	The Limit of detection using calibration control (artificial DNA) was down to: § EYA4: 0.18% § GRIA4: 0.18% § ITGA4: 0.09% § MAP3K14-AS1: 0.18% § MSC: 0.09%
Mean copies per partition	The average number of events over all tissue samples assessed were: - EYA4: 9767 events - GRIA4: 5995 events \ - ITGA4: 4603 events - MAP3K14-AS1: 9308 events - MSC: 7846 events The average number of events over all cfDNA samples assessed were: - EYA4: 18939 events - GRIA4: 11401 events \ - ITGA4: 3677 events - MAP3K14-AS1: 15963 events - MSC: 16584 events In the prevalence dataset only comparing normal self-declared healthy samples (H) from cancer samples (C): - EYA4: H= 8560 events – C= 20594 - GRIA4: H= 4464 events – C= 12562 - ITGA4: H= 2590 events – C= 3855 - MAP3K14-AS1: H= 4715 events – C= 17798 - MSC: H= 9216 events – C= 17777
dPCR analysis program (source, version)	BD Accuri C6 software Version 1.0.264.21
Outlier identification and disposition.	Non amplified samples were amplified a 3rd time and in case of failure were annotated as NA. Replicates with more than 20% variation in cfDNA were re-amplified.
Results of no-template controls	No-template control had to show less than 100 cumulated events (Methylated and Unmethylated), or the run was reperformed.
Examples of positive(s) and negative experimental results	For each graph: R5 Unmethylated events; R4 Methylated Events; R6 Empty Beads. - Fully methylated sample:

<table>
<tr><td></td><td>


- Intermediate methylation: (37.1%)


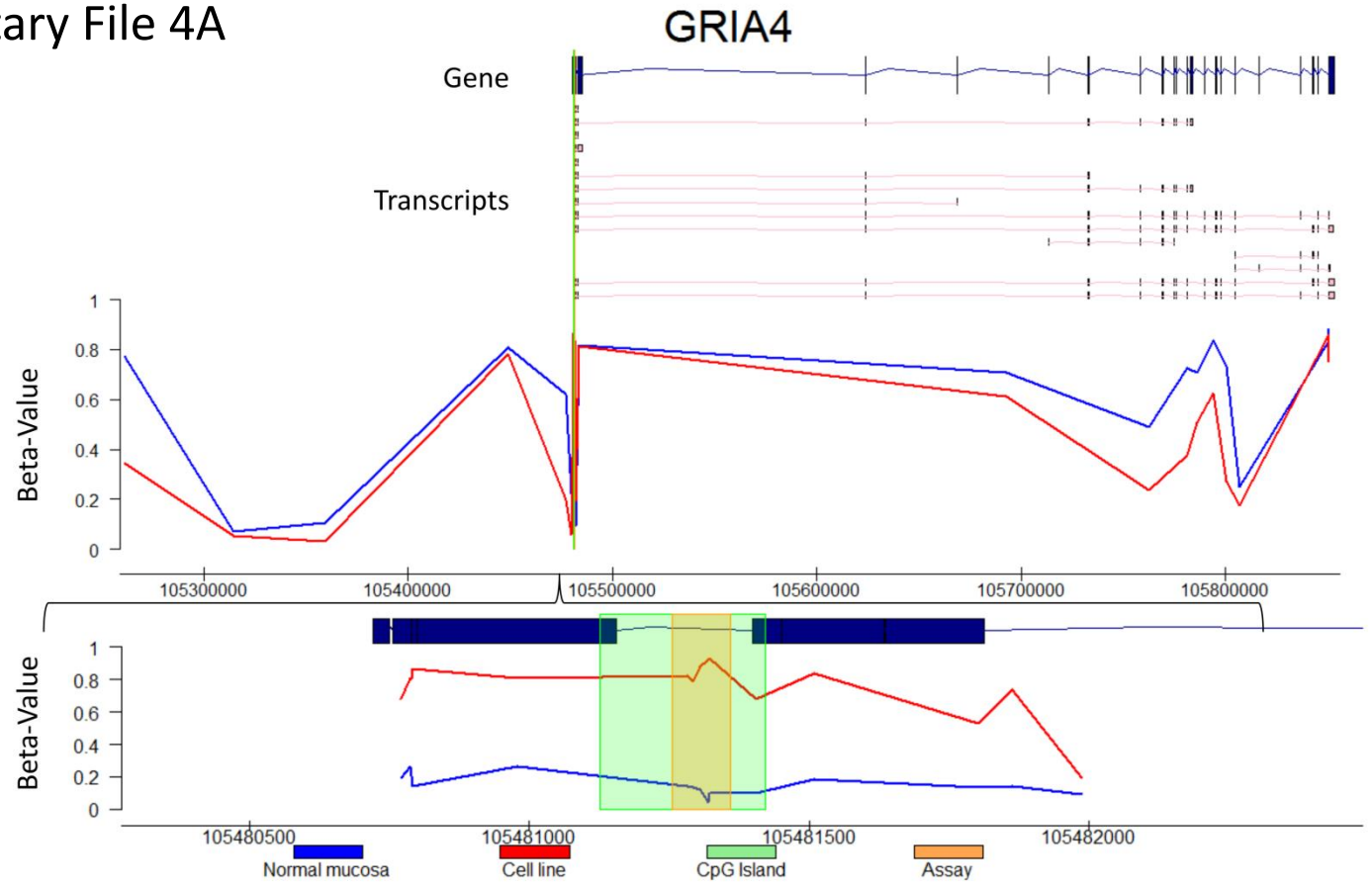
- Fully unmethylated:


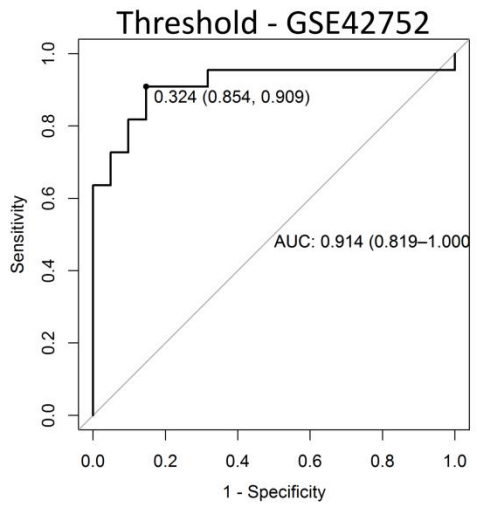
</td></tr>
<tr><td>normalization method</td><td>Percentage of methylation was calculated on the number of events obtained in the methylated gate (R4) / number of cumulated events (events in methylated (R4) and unmethylated gate (R5)).
$$Methylation\ value = \frac{R4}{(R4 + R5)} X\ 100$$</td></tr>
<tr><td>biological replicates</td><td>Not applicable.</td></tr>
<tr><td>Number and stage of technical replicates.</td><td>Replication was performed at the 1st amplification stage.
i.e. 1 plasma / tissue sample → 1 DNA → 1 BisDNA → 2 1st PCR /assay → 2 EmPCR /assay → 2 well in FACs.</td></tr>
<tr><td>Repeatability</td><td>The repeatability was assessed for tissue and cfDNA separately, considering the</td></tr>
</table>

<table>
<tr>
<td>(intraassay variation) & Experimental variance</td>
<td>average standard deviation [± SD] on all assessed samples:
- In tissue DNA:
§ EYA4: 4.36 % [± 2.84]
§ GRIA4: 3.72 % [± 3.08]
§ ITGA4: 2.97 % [± 2.47]
§ MAP3K14-AS1: 3.24 % [± 3.14]
§ MSC: 5.61 [± 4.67]
- In cfDNA:
§ EYA4: 3.29 % [± 4.24]
§ GRIA4: 4.07 % [± 4.78]
§ ITGA4: 3.72 % [± 4.70]
§ MAP3K14-AS1: 3.05 % [± 4.19]
§ MSC: 2.90 % [± 4.26]</td>
</tr>
<tr>
<td>Limit of blank</td>
<td> 

The limit of blank was calculated using the negative template samples which displayed some output and on five ultramer samples corresponding to the fully unmethylated template. Since the distribution of the false events does not always follow a Poisson distribution, an empirical estimate for the 95% upper confidence limit of the data was estimated (as applied in Taly et al. Clin Chem 2013):
<table>
<tr><th></th><th>N</th><th>λ</th><th>LOB (Poisson)</th><th>LOB (empirical)</th></tr>
<tr><td>EYA4</td><td>28</td><td>3.6</td><td>5</td><td>6</td></tr>
<tr><td>GRIA4</td><td>30</td><td>1.7</td><td>3</td><td>3</td></tr>
<tr><td>ITGA4</td><td>27</td><td>1.5</td><td>2</td><td>3</td></tr>
<tr><td>MAP3K14-AS1</td><td>29</td><td>1.9</td><td>3</td><td>3</td></tr>
<tr><td>MSC</td><td>30</td><td>2.4</td><td>3</td><td>4</td></tr>
</table>
</td>
</tr>
</table>

Suplementary File 4A

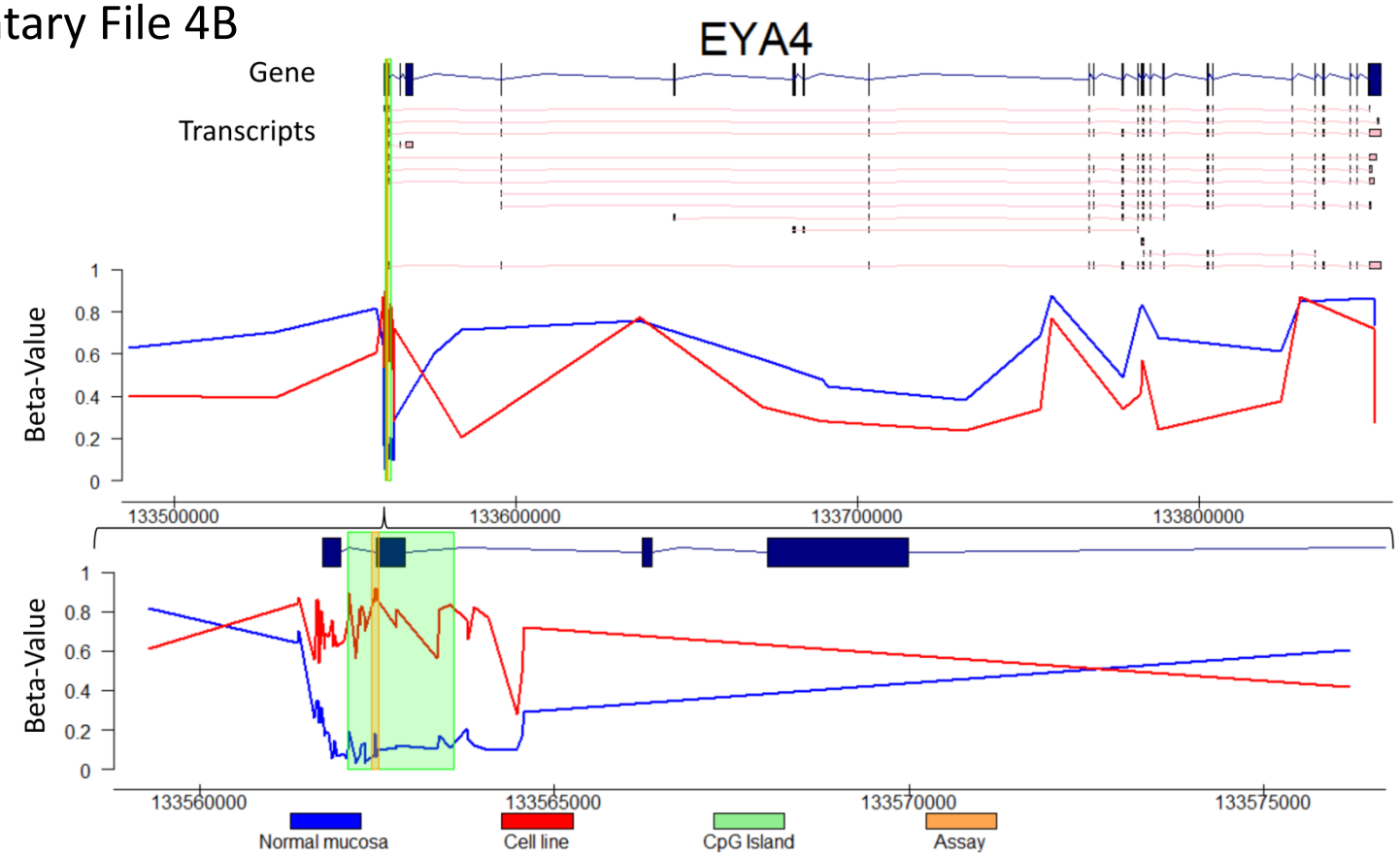


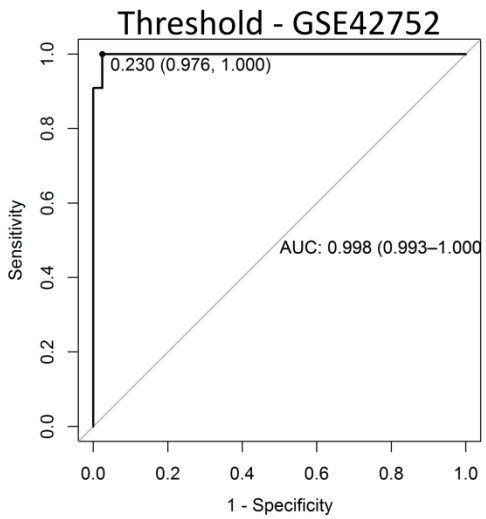


TCGA COREAD

p-value < 2e-16	**<0.324**	**>0.324**	NPV	PPV
Normal	45	0	0.7	1
Cancer	16	399		

Suplementary File 4B

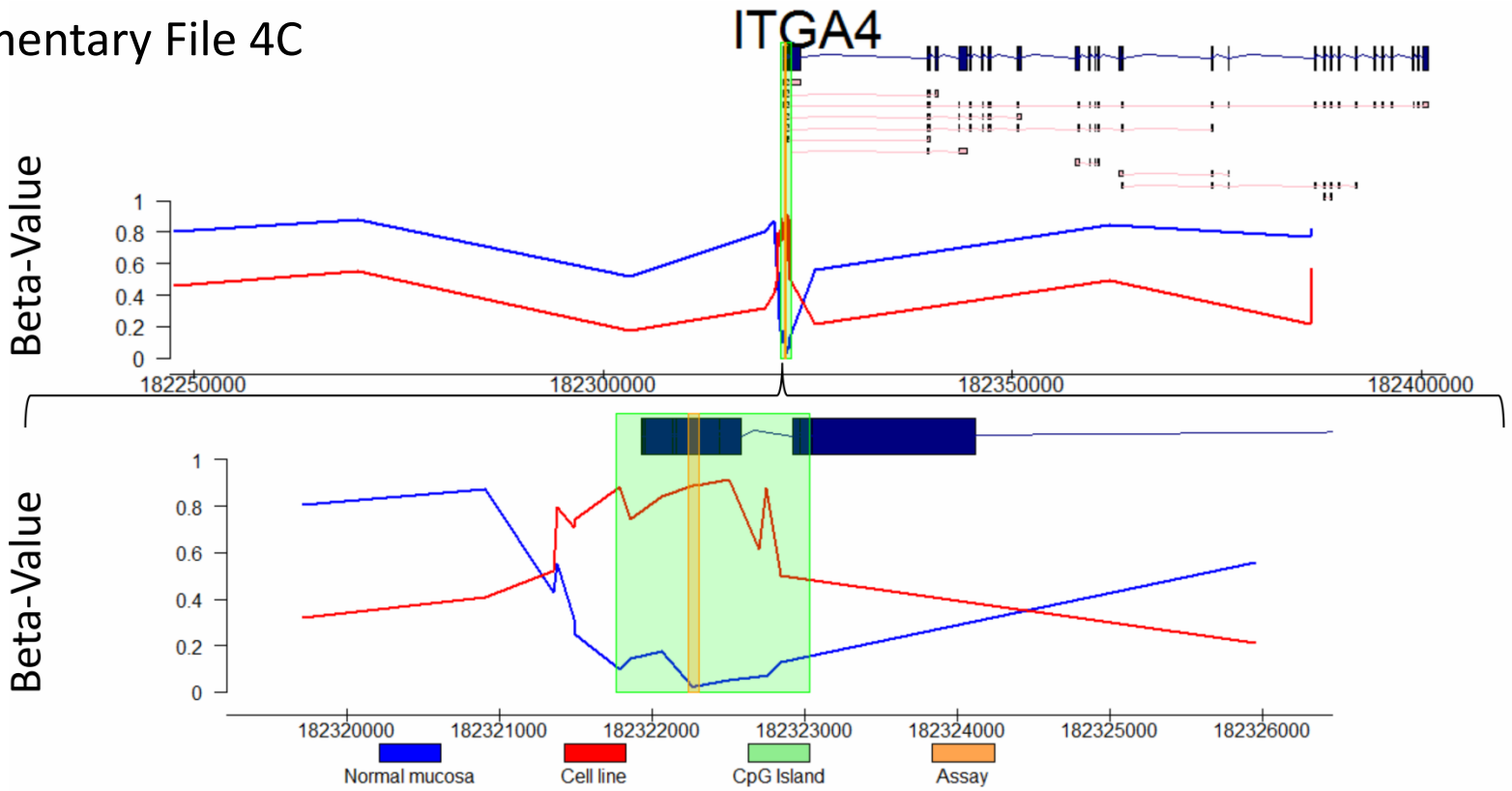


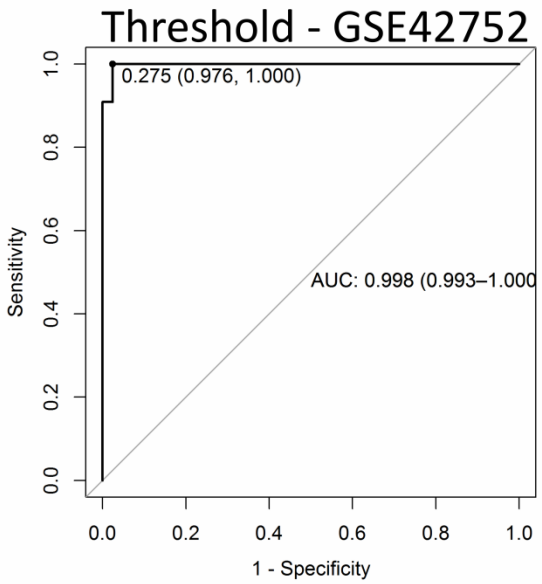


TCGA COREAD

p-value < 2e-16	**<0.230**	**>0.230**	NPV	PPV
Normal	45	0	0.6	1
Cancer	26	389		

Suplementary File 4C

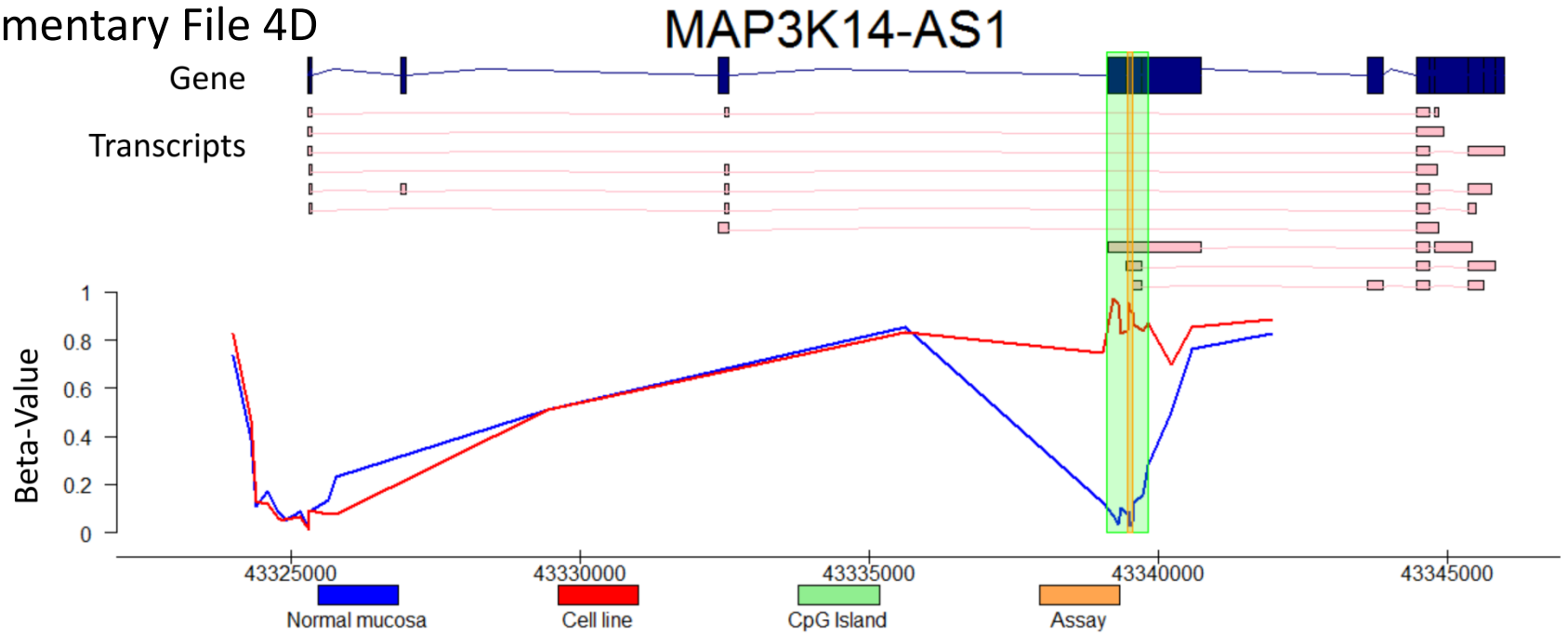


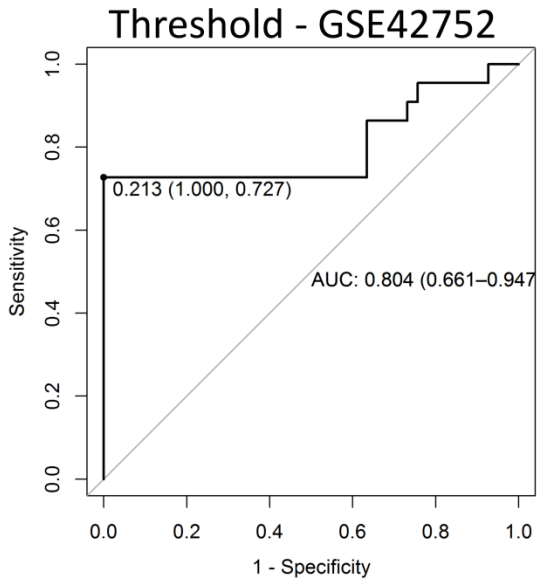


TCGA COREAD

p-value < 2e-16	**<0.275**	**>0.275**	NPV	PPV
Normal	45	0	0.8	1
Cancer	9	403		

Suplementary File 4D

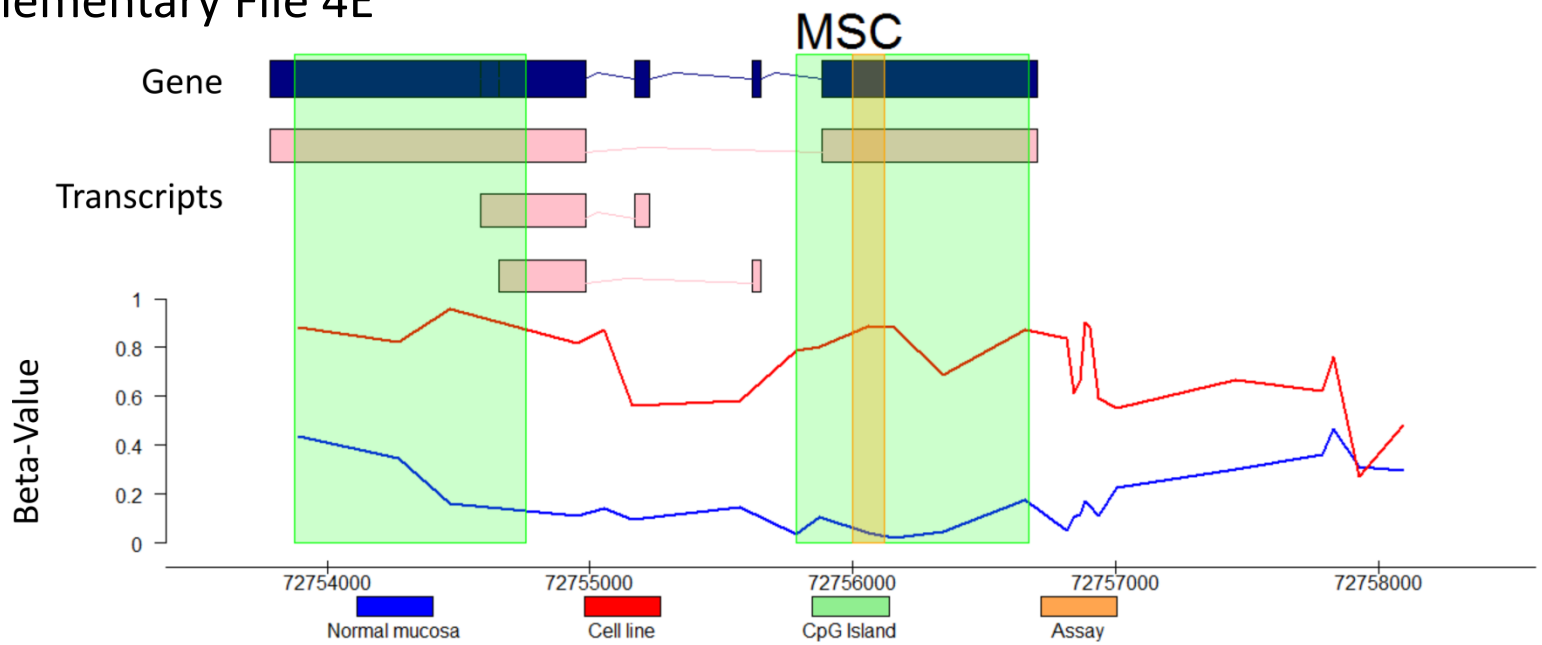


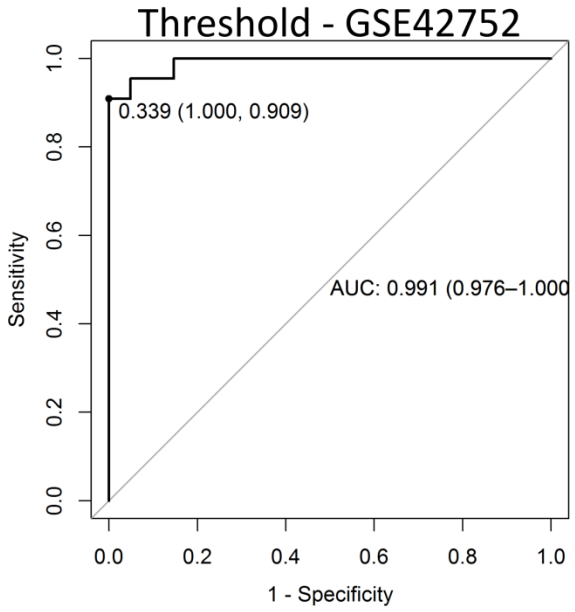


TCGA COREAD

p-value < 2e-16	**<0.213**	**>0.213**	NPV	PPV
Normal	45	0	0.5	1
Cancer	39	376		

Suplementary File 4E

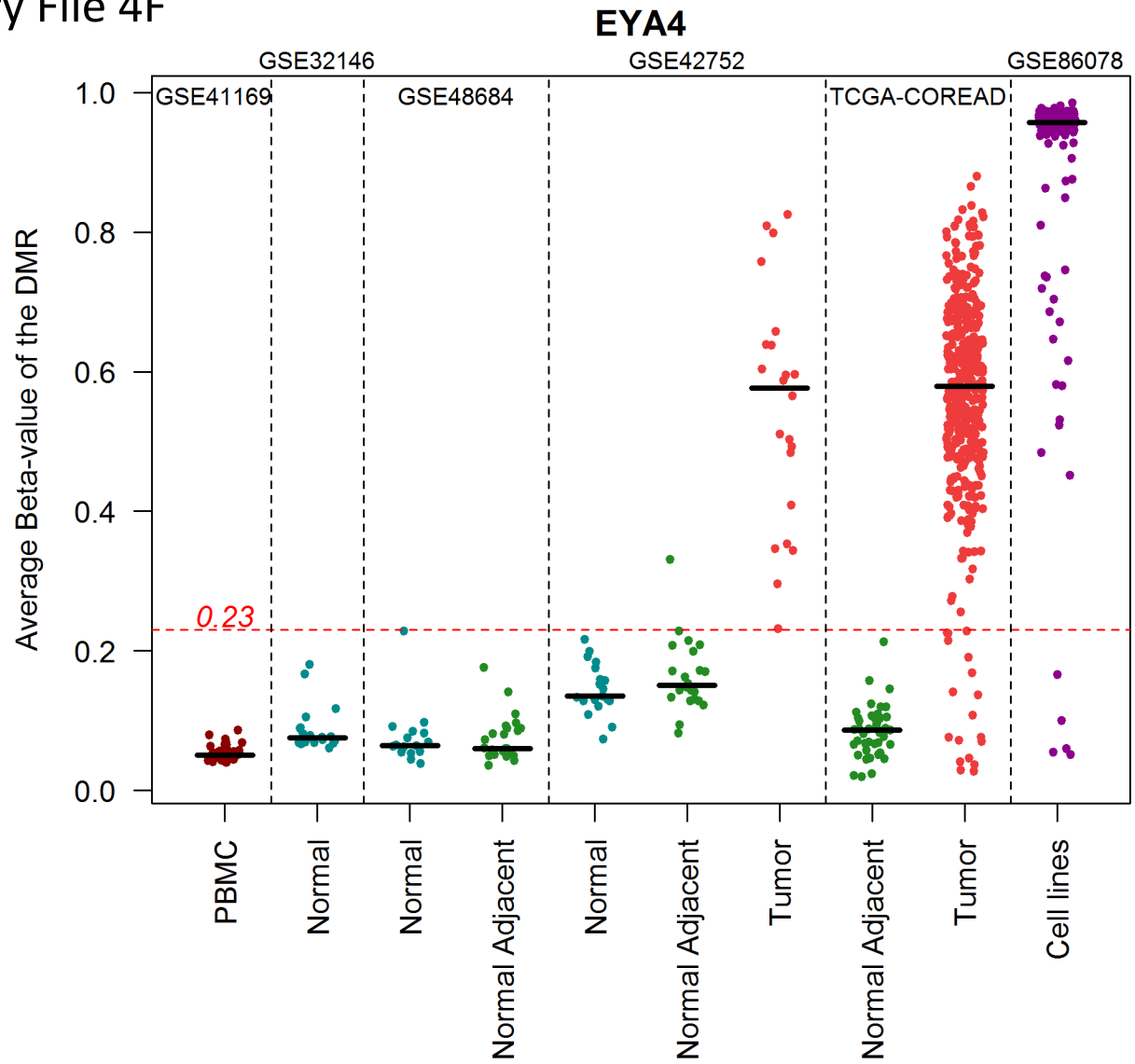




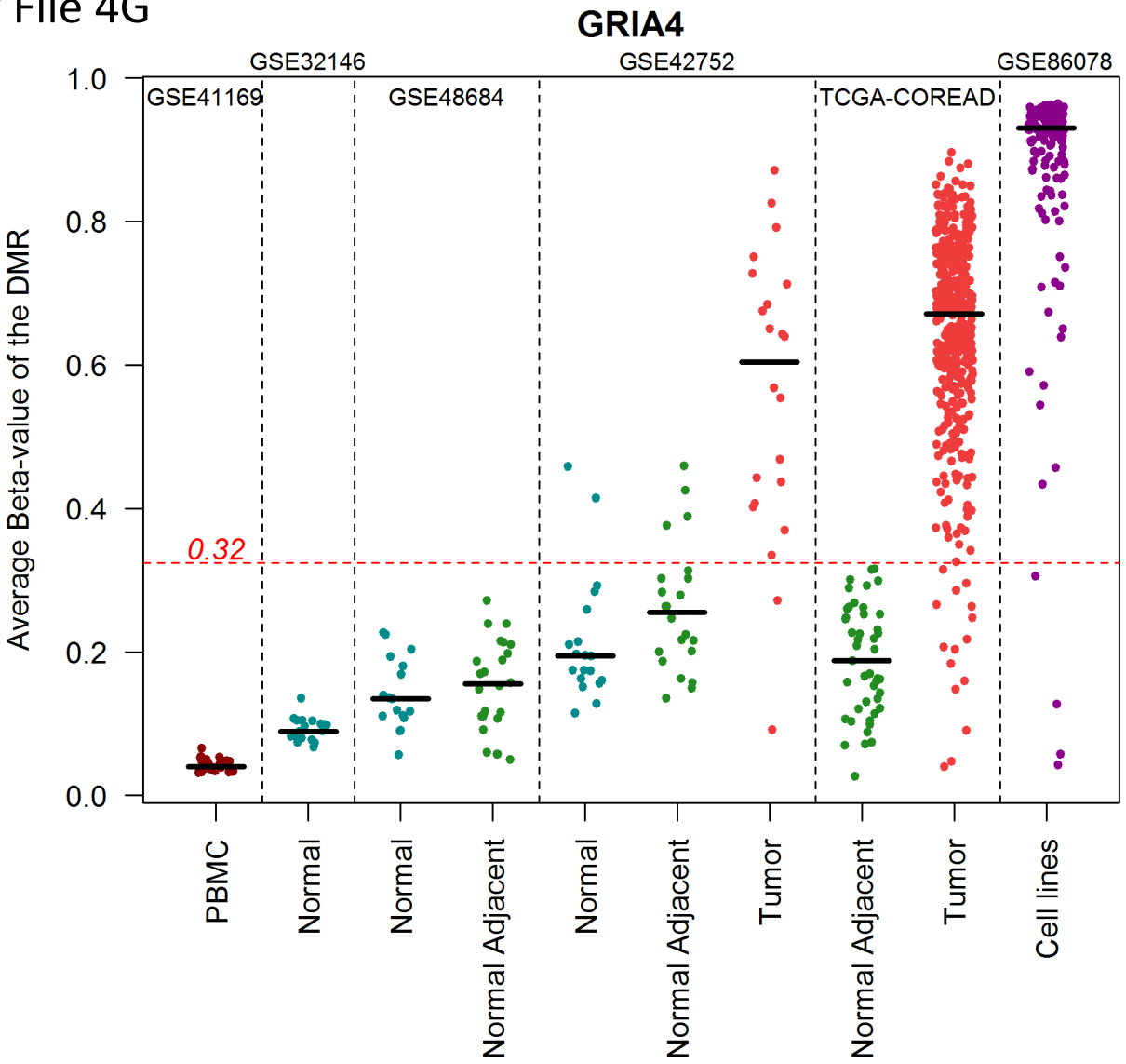
TCGA COREAD

p-value < 2e-16	**<0.339**	**>0.339**	NPV	PPV
Normal	45	0	0.7	1
Cancer	19	396		

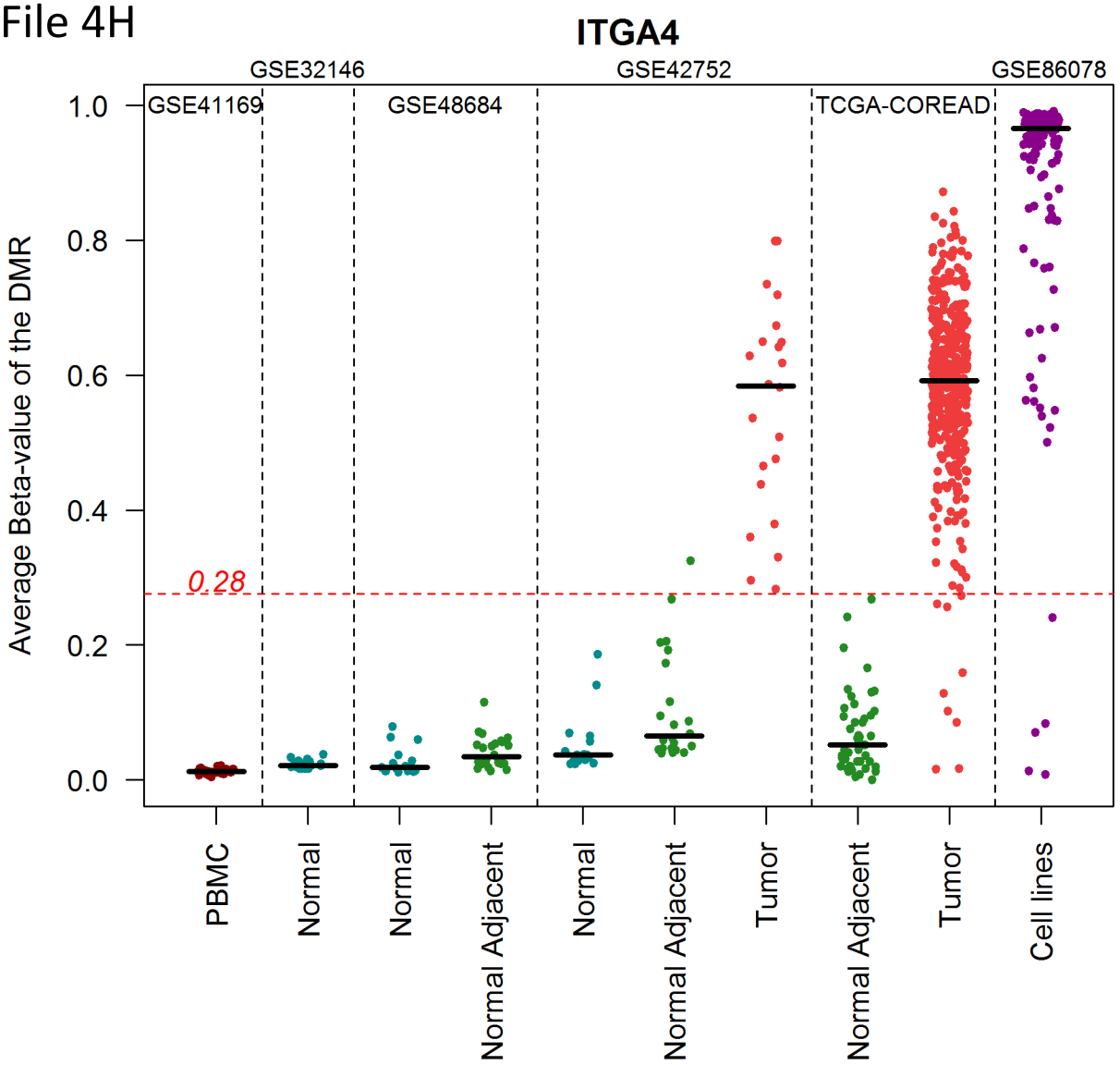
Suplementary File 4F



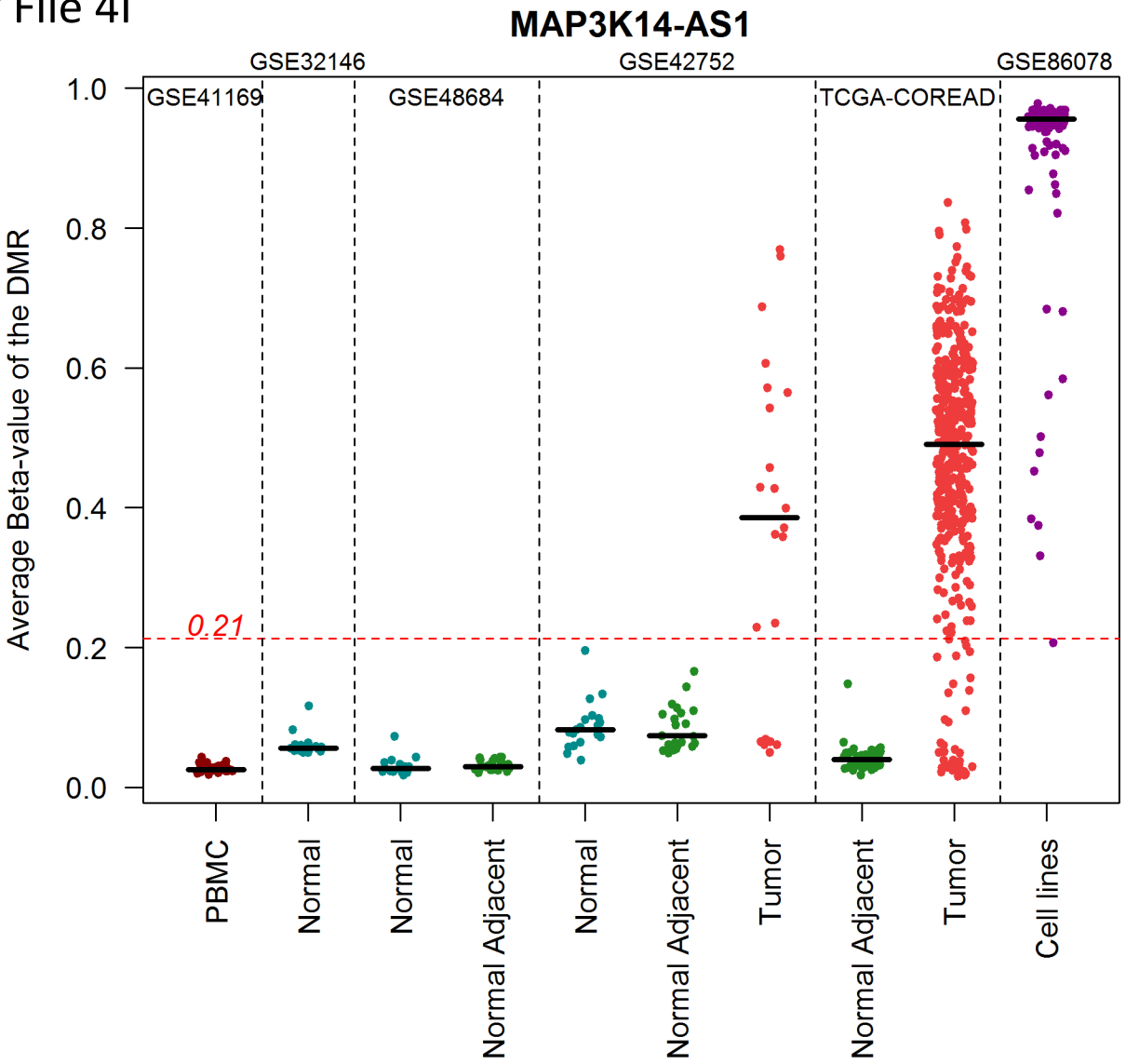
Suplementary File 4G



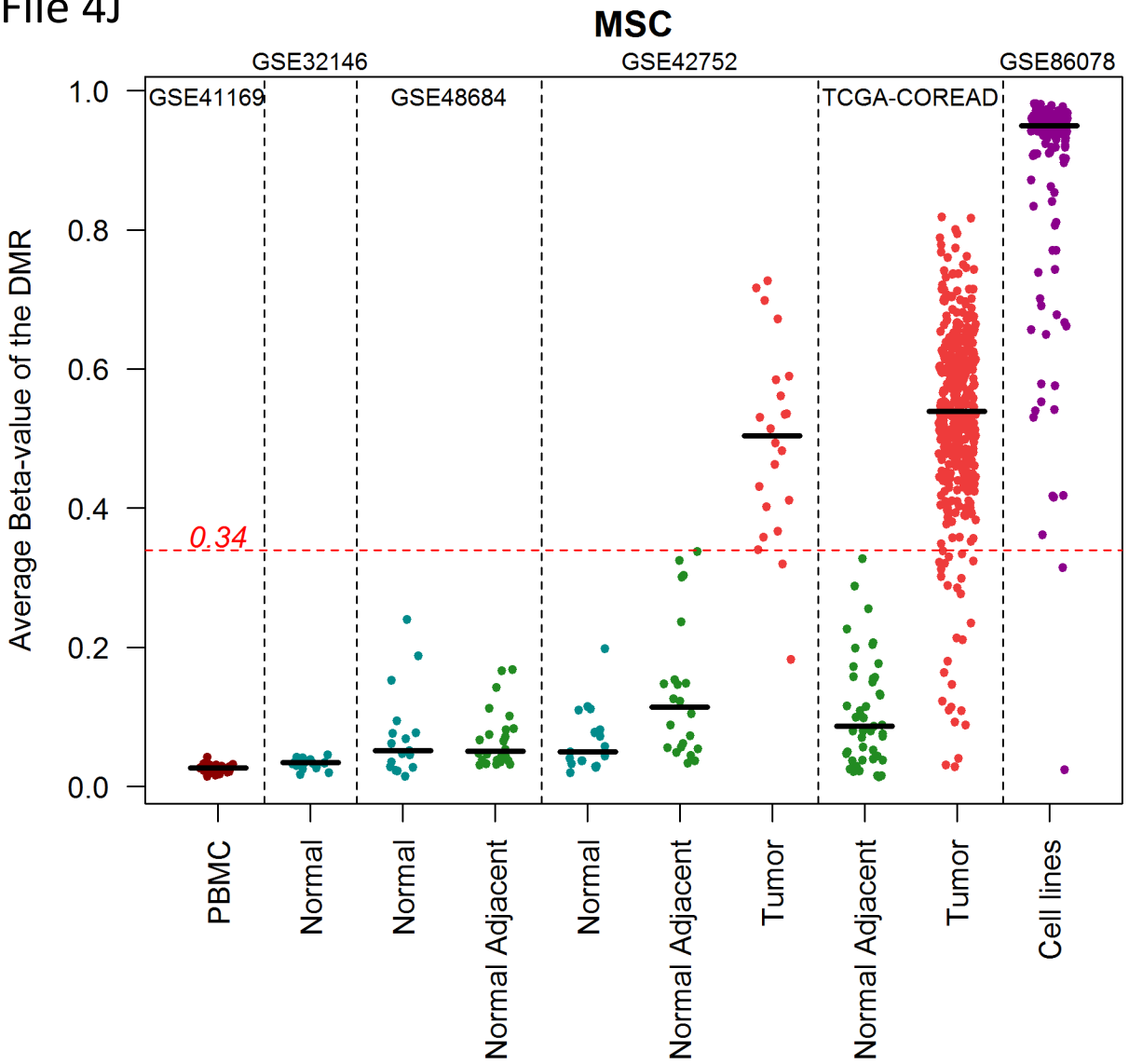
Suplementary File 4H



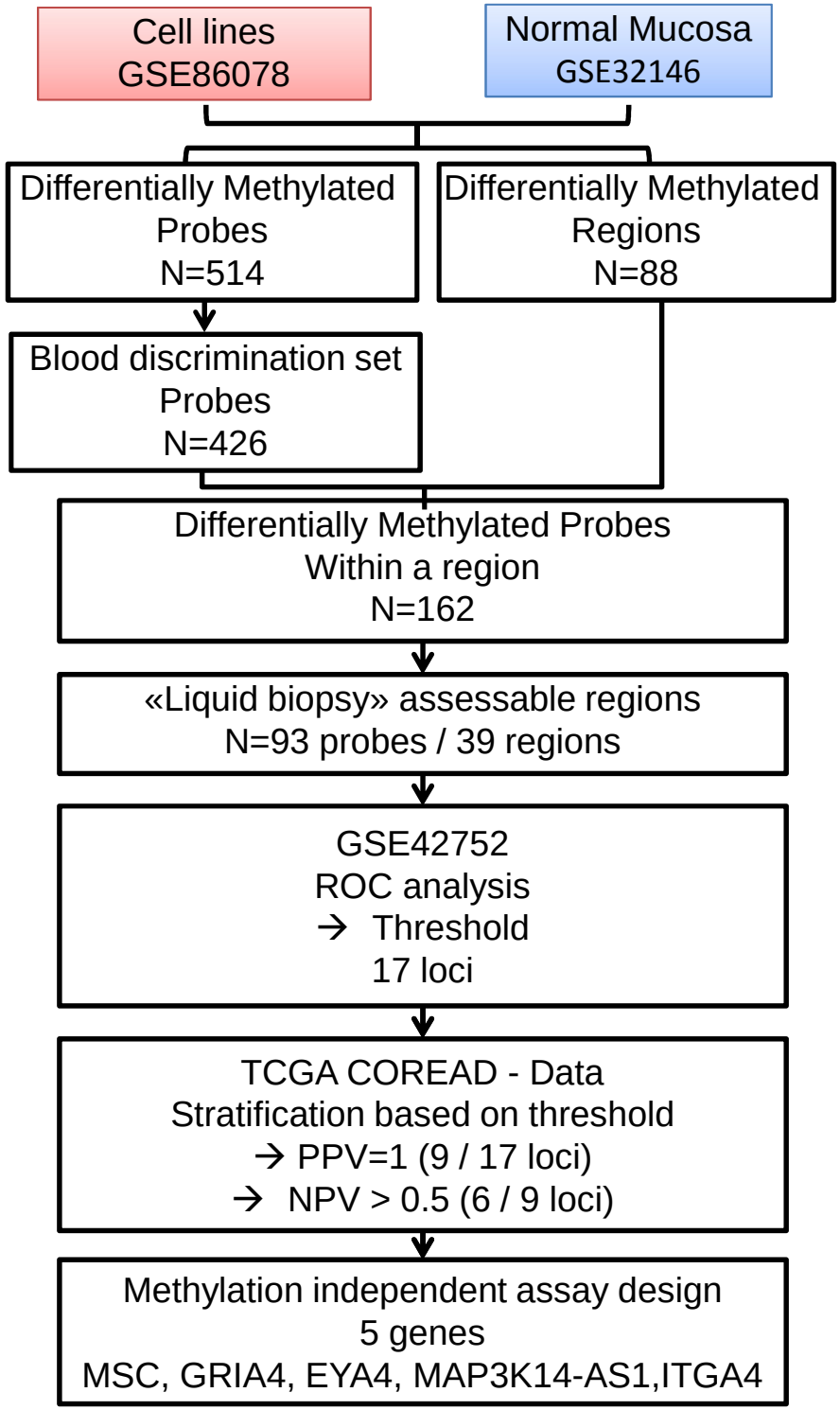
Suplementary File 4l



Suplementary File 4J



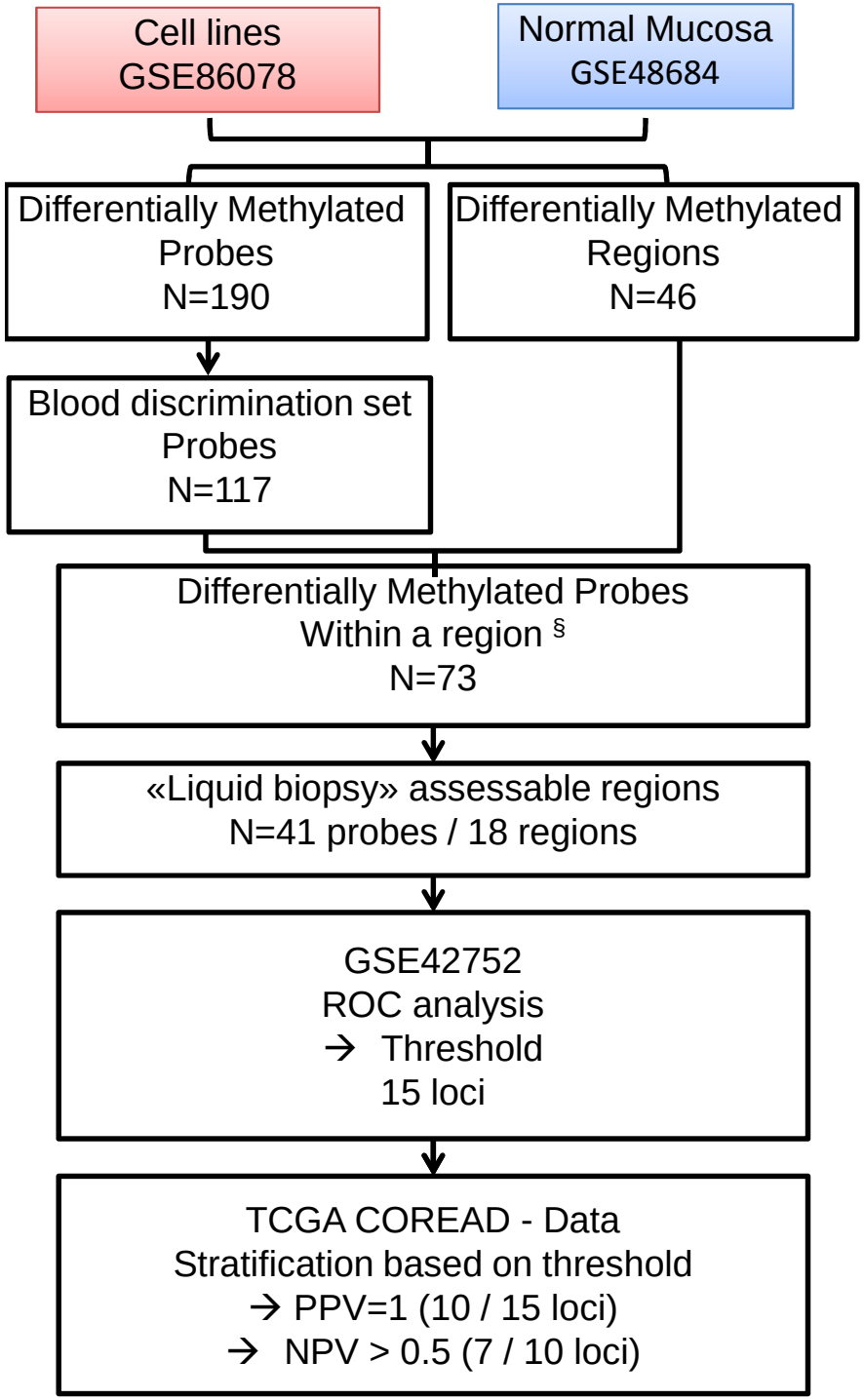
Supplementary File 5A



gene	seqnames	start	end	threshold	NPV	PPV
DAB1	chr1	58715539	58715553	0.42	0.500	0.997
SPAG6	chr10	22634432	22634439	0.31	0.495	1.000
KIAA1217	chr10	23983496	23983498	0.15	0.683	0.990
TLX1	chr10	102893980	102894120	0.38	0.600	1.000
INA	chr10	105036701	105036727	0.40	0.425	1.000
NELL1-A	chr11	20690720	20690807	0.27	0.829	0.974
NELL1-B	chr11	20691126	20691161	0.40	0.672	0.990
MIR129-2	chr11	43602845	43602879	0.36	0.592	1.000
GRIA4	chr11	105481317	105481322	0.26	0.714	1.000
DDX25	chr11	125774082	125774092	0.51	0.402	0.973
TM6SF1	chr15	83776269	83776420	0.27	0.543	0.997
BNC1	chr15	83952345	83952420	0.35	0.632	0.995
SALL1	chr16	51185001	51185082	0.38	0.542	1.000
C17orf46*	chr17	43339223	43339328	0.26	0.584	1.000
LOC100133991*	chr17	43339497	43339589	0.21	0.549	1.000
CLIP4-A	chr2	29338077	29338121	0.50	0.735	0.978
CLIP4-B	chr2	29338113	29338258	0.52	0.706	0.978
OTX1-A	chr2	63281069	63281139	0.20	0.409	1.000
OTX1-B	chr2	63283967	63284066	0.11	0.405	1.000
OTX1-C	chr2	63284066	63284132	0.13	0.415	0.997
CNRIP1	chr2	68546467	68546579	0.31	0.732	0.990
ITGA4	chr2	182322268	182322279	0.28	0.833	1.000
THBD	chr20	23029287	23029298	0.49	0.433	1.000
SLC32A1	chr20	37353096	37353126	0.45	0.423	0.997
TRH	chr3	129693489	129693586	0.42	0.657	0.997
PEX5L	chr3	179754603	179754613	0.41	0.412	0.992
TMEM155	chr4	122686453	122686493	0.40	0.579	0.997
MARCH11	chr5	16180033	16180076	0.47	0.254	1.000
SPOCK1	chr5	136834464	136834492	0.45	0.463	0.997
UBD	chr6	29521751	29521756	0.41	0.662	1.000
EYA4	chr6	133562461	133562492	0.23	0.714	1.000
SND1-A	chr7	127672473	127672564	0.30	0.977	0.995
SND1-B	chr7	127672564	127672658	0.34	0.977	0.995
FAM115A	chr7	143579665	143579698	0.53	0.652	1.000
NEFM	chr8	24772350	24772435	0.37	0.258	0.983
PLAG1	chr8	57069907	57070013	0.36	0.652	0.995
ADHFE1	chr8	67344665	67344720	0.46	0.714	1.000
TCF24	chr8	67874178	67874206	0.17	0.484	0.997
MSC	chr8	72756058	72756155	0.35	0.662	1.000

* same gene locus MAP3K14-AS1

Supplementary File 5B

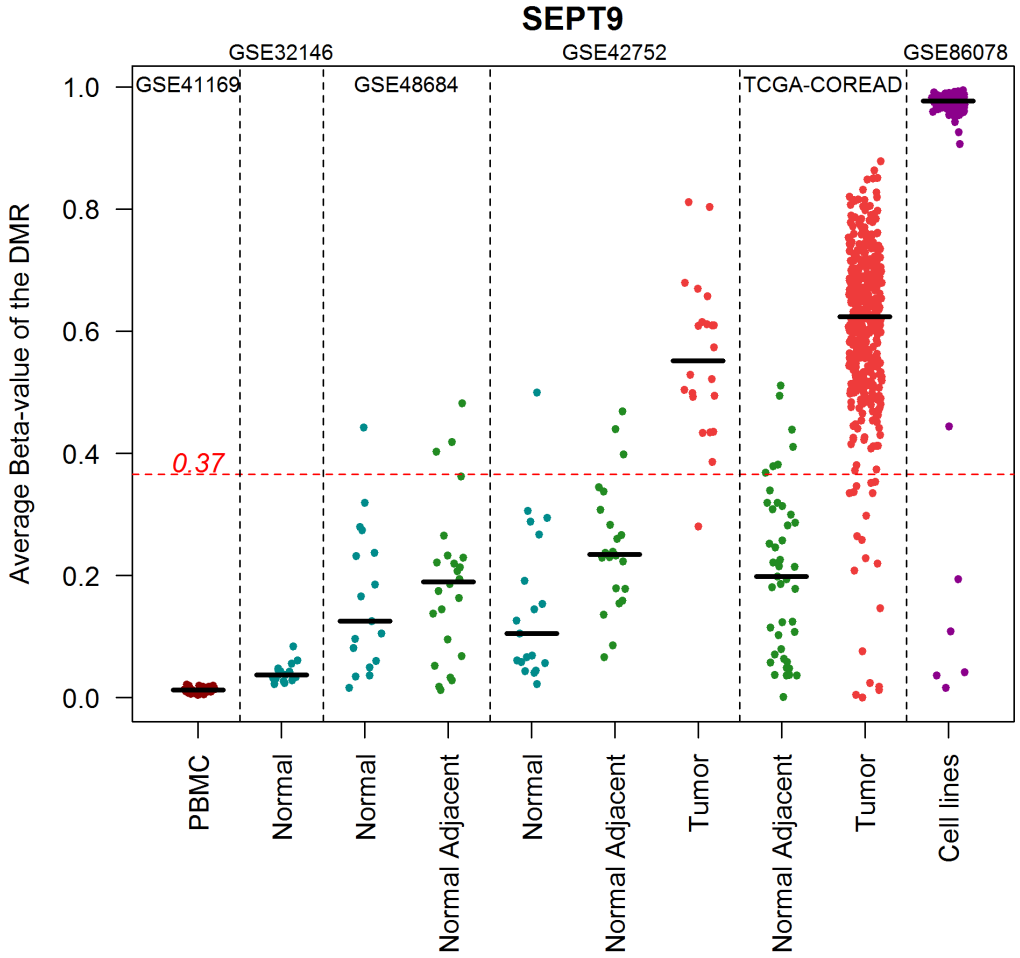


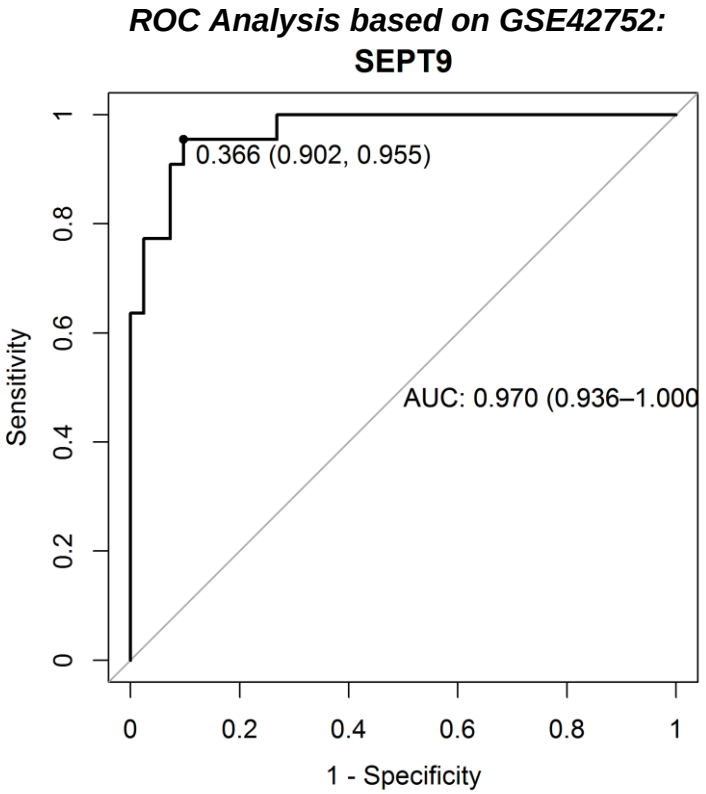
	seqnames	start	end	threshold	NPV	PPV
SPAG6	chr10	22634432	22634439	0.312	0.495	1.000
KIAA1217	chr10	23983496	23983498	0.148	0.683	0.990
GRIA4	chr11	105481317	105481322	0.258	0.714	1.000
C17orf46*	chr17	43339223	43339328	0.262	0.584	1.000
LOC100133991*	chr17	43339497	43339589	0.208	0.549	1.000
OTX1-A	chr2	63283967	63284066	0.114	0.405	1.000
OTX1-B	chr2	63284066	63284132	0.126	0.415	0.997
NXPH2	chr2	139537824	139537845	0.382	0.662	1.000
ITGA4	chr2	182322268	182322279	0.275	0.833	1.000
COL25A1	chr4	110223795	110223830	0.240	0.600	1.000
MARCH11	chr5	16180033	16180055	0.304	0.409	1.000
UBD-A	chr6	29521138	29521143	0.360	0.563	1.000
UBD-B	chr6	29521568	29521595	0.282	0.672	1.000
EYA4	chr6	133562479	133562492	0.199	0.738	1.000
SND1-A	chr7	127672169	127672235	0.095	0.657	0.997
SND1-B	chr7	127672473	127672564	0.304	0.977	0.995
ADHFE1	chr8	67344665	67344720	0.461	0.714	1.000
TCF24	chr8	67874178	67874206	0.169	0.484	0.997

* same gene locus MAP3K14-AS1

§ Loss of MSC region due to presence of only one significant DMP

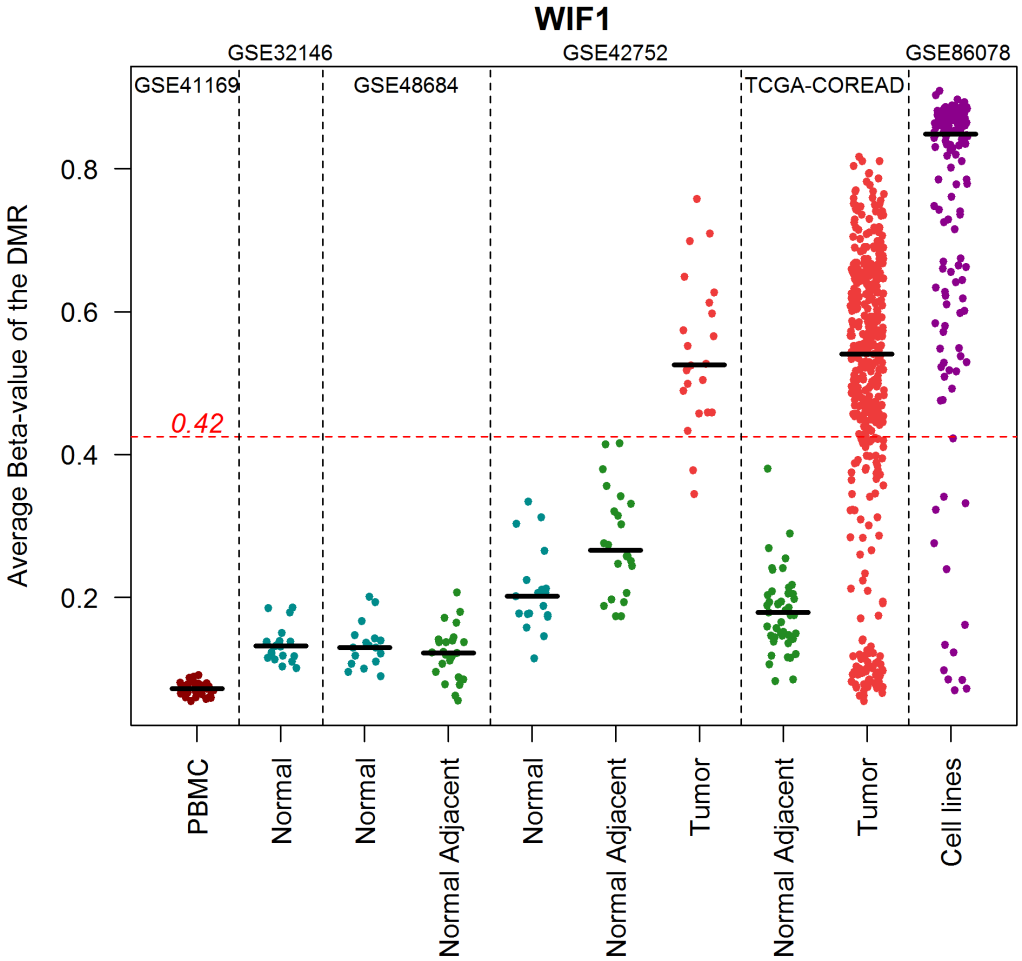
Supplementary File 6A

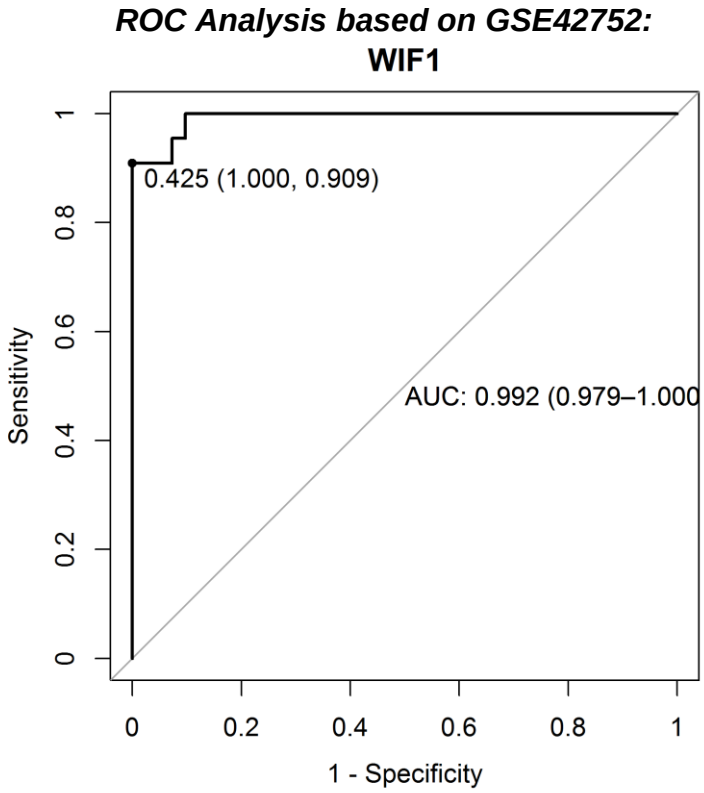




Region Assessed: Hg19: chr17: 75369484-75369657
Overlapping Probes: cg20275528; cg12783819
Exclusion criteria: DMP too far away >150bp.

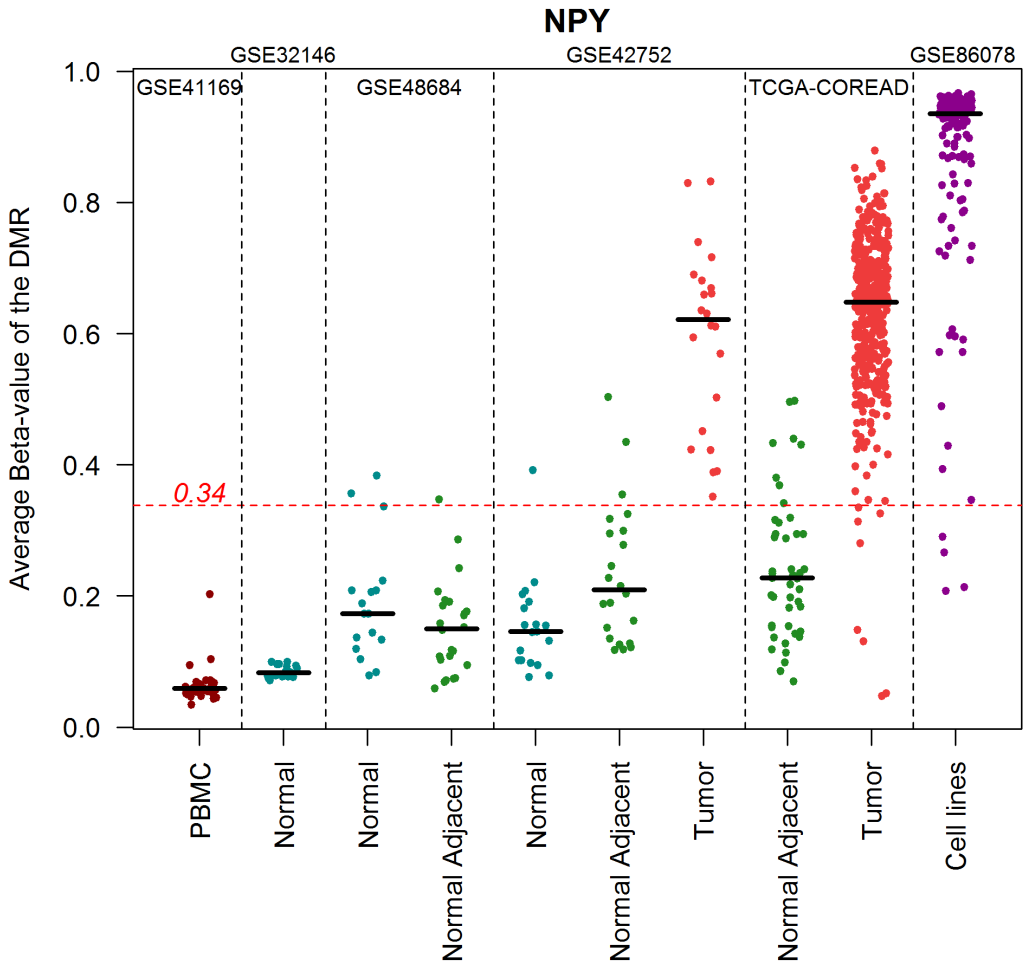
Supplementary File 6B

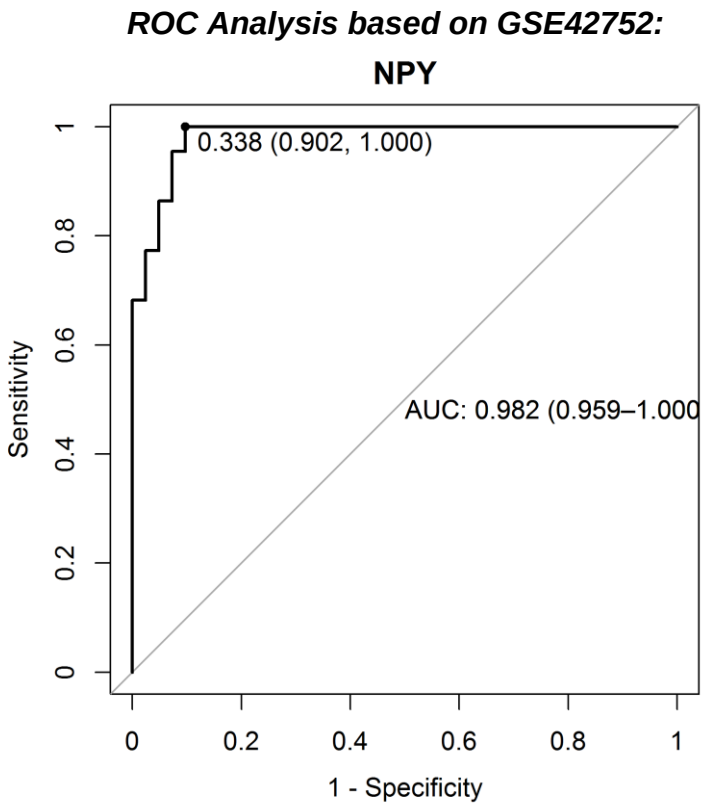




Region Assessed: Hg19:chr12:65514979-65515037 (assessed by Roperch *et al. BMC Cancer 2013*)
Overlapping Probes: cg03509412; cg19427610; cg26733786.
Exclusion criteria: differential methylation value below the 0.8 beta-value threshold; threshold established in GSE42752 above the 0.35 cut-off.

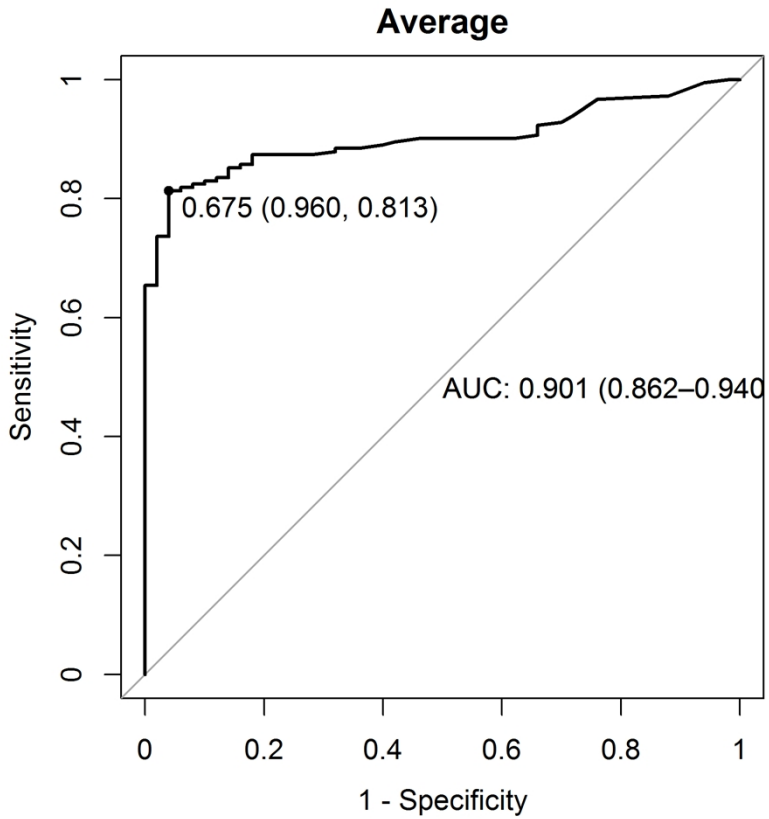
Supplementary File 6C

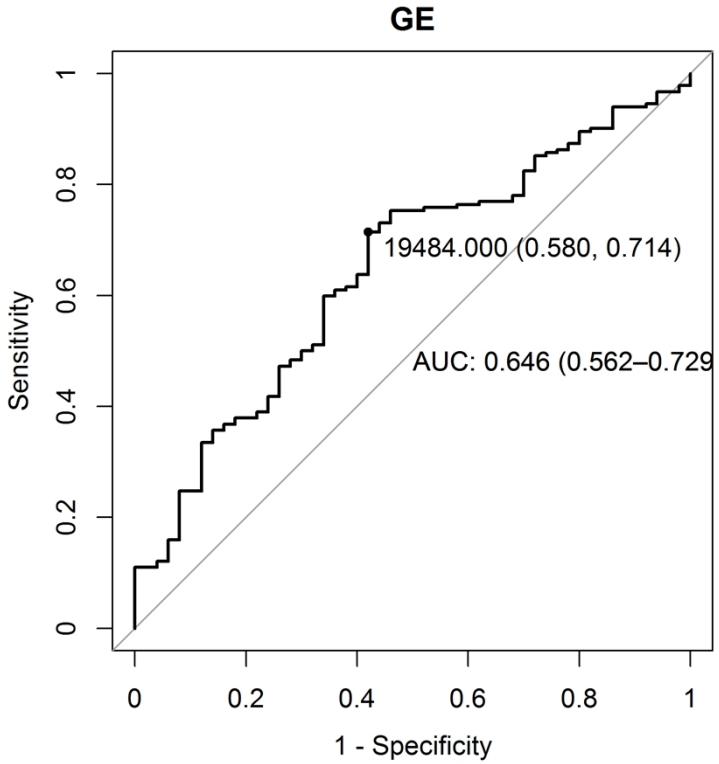


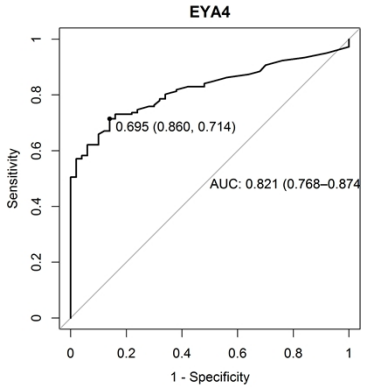


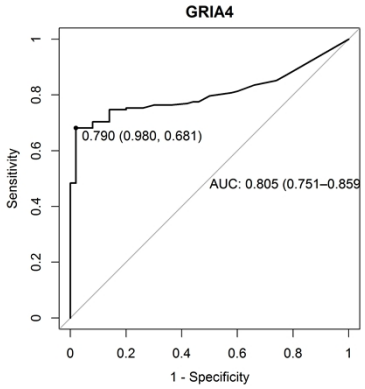
Region Assessed: Hg19:chr7:24323761-24323856 (assessed by Roperch *et al. BMC Cancer 2013*)
Overlapping Probes: cg24885417; cg00355281; cg15929698; cg16964348; cg25884711.
Exclusion criteria: positivity in blood (GSE41169) and multiple positive normal healthy and normal peritumoural tissue samples (yielding a specificity <1 in the validation cohort).

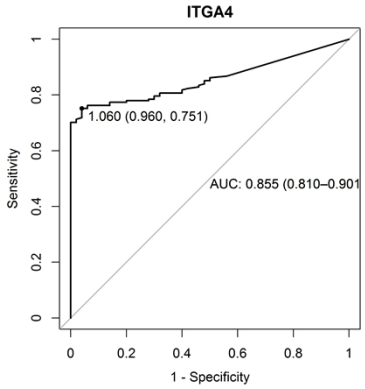
Supplementary File 7

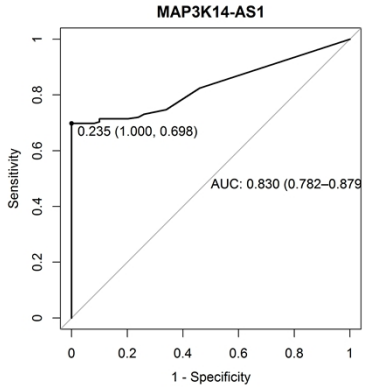


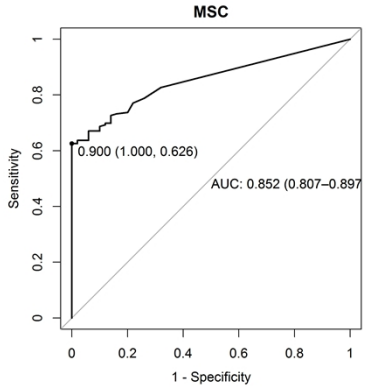




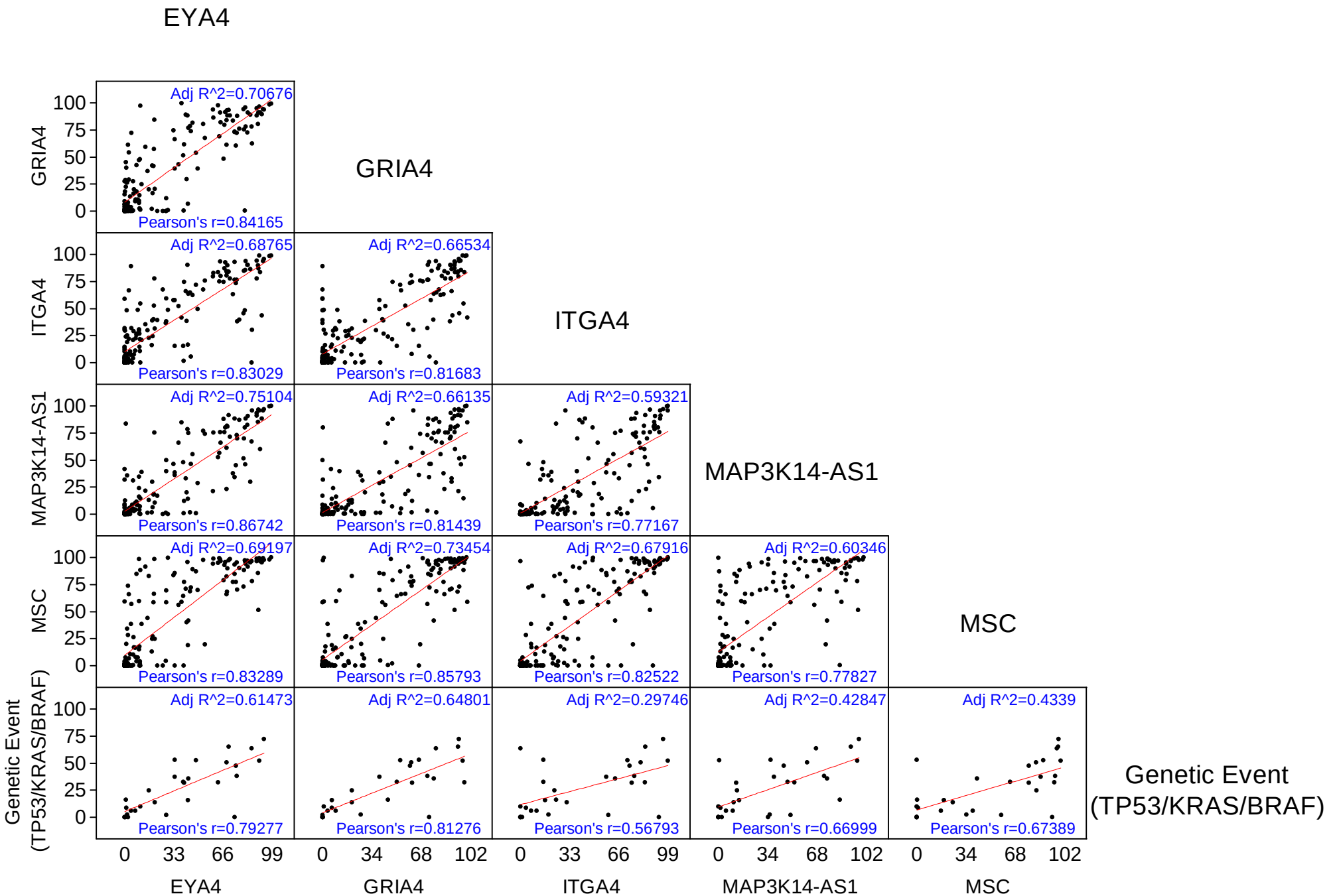




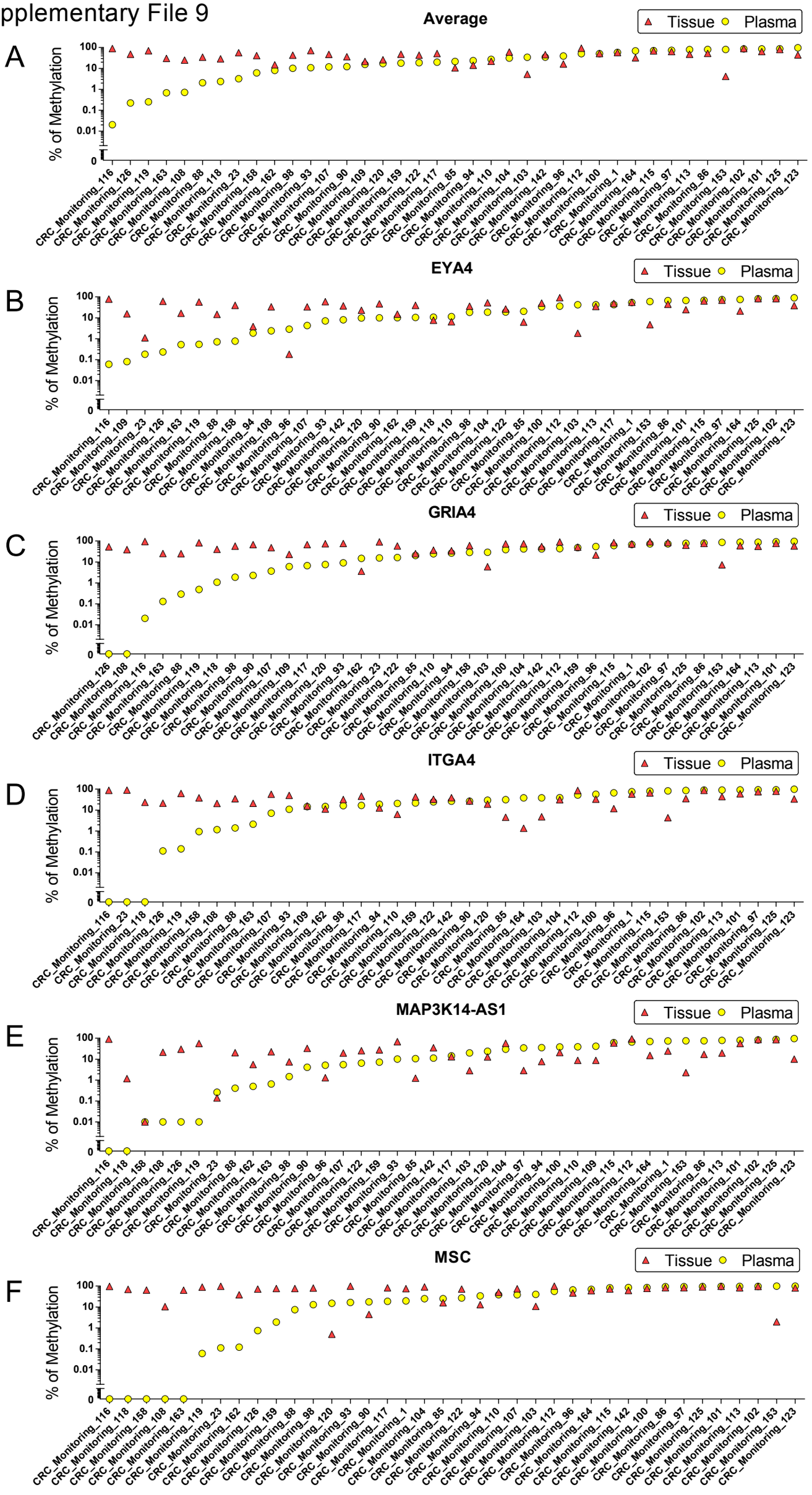




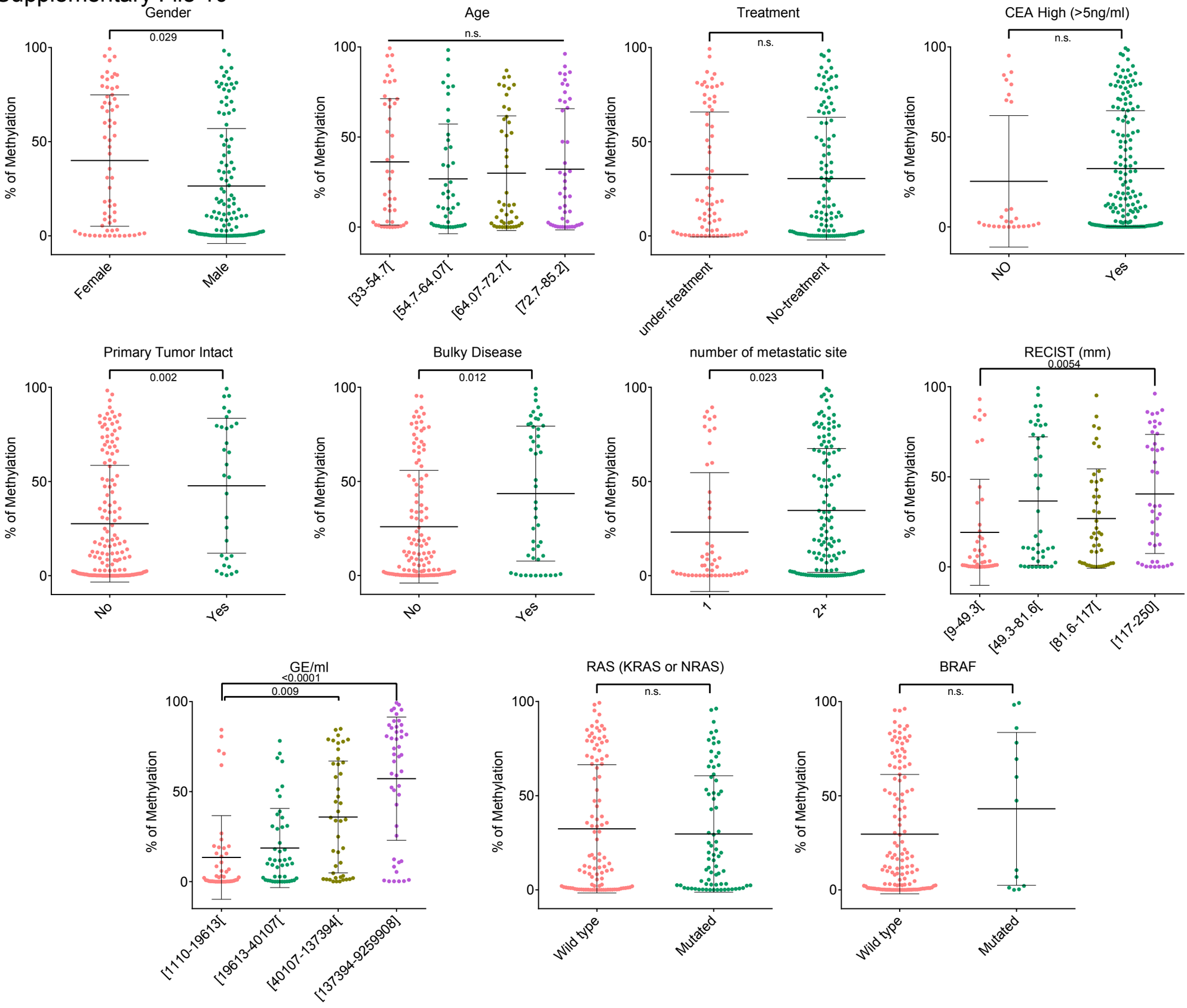
Supplementary File 8



Supplementary File 9



Supplementary File 10



Supplementary File 11